

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: February 12, 2003, 16:35:15 ; Search time 50 Seconds

(without alignments)  
134.383 Million cell updates/sec

Title: US-09-677-374-2

Perfect score: 836  
Sequence: 1 MNRGCGSSLIISVFLVG.....IYGFACROPGRMQUISTEK 162

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	296	35.4	159	17KD_RICPR	P16624 rickettsia
2	294	35.2	159	17KD_RICJA	O52764 rickettsia
3	293	35.0	159	17KD_RICCN	P05372 rickettsia
4	284.5	34.0	159	17KD_RICRY	P22882 rickettsia
5	276	33.0	154	17KD_RICAU	P50928 rickettsia
6	263	31.5	154	17KD_RICAM	P50927 rickettsia
7	261	31.2	154	17KD_RICPA	P50930 rickettsia
8	261	31.2	154	17KD_RICRH	P50931 rickettsia
9	258	30.9	154	17KD_RICMO	P50929 rickettsia
10	157	18.8	80	17KD_RICCA	P29697 rickettsia
11	113.5	13.6	155	PCP_YEREN	P31484 yersinia
12	105.5	12.6	155	SLVB_ECOLI	P55741 escherichia
13	103.5	12.6	155	SLVB_SALTY	O53349 salmonella
14	102	12.2	155	PCP_HAEIN	P10325 haemophilus
15	99	11.8	179	YCFJ_ECOLI	P37796 escherichia
16	98	11.7	172	YFGB_ECOLI	P76572 escherichia
17	90	10.8	526	KICJ_BOVIN	P06394 bos taurus
18	90	10.8	1332	KICD_BOVIN	P54334 bacillus su
19	89	10.6	1583	YQBO_BACSU	P45331 bacillus su
20	87.5	10.3	72	OSMB_SALTY	P37723 salmonella
21	86.5	10.3	72	OSMB_ECOLI	P17873 escherichia
22	84.5	10.1	243	CYSH_SALTY	P17853 salmonella
23	84.5	10.1	301	STXG_RAT	O92158 rattus norv
24	84.5	10.1	431	KR22_CANAL	O00310 candida alb
25	84.5	10.1	526	VPS_BTVI1	P33476 bluetongue
26	83.5	10.0	243	CYSH_SALTY	O82460 salmonella
27	82	9.8	132	Y615_AQUAE	O66867 aquifex aeo
28	82	9.8	263	CANS_BOVIN	P13135 bos taurus
29	81.5	9.7	541	NUS7_YEAST	P48837 saccharomyc
30	81.5	9.7	747	SPD1_NEPCL	P19837 nephila cia
31	80.5	9.6	467	HEML_MYCLE	P46724 mycobacteri
32	79.5	9.5	266	CANS_RABIT	P06613 oryctolagus
33	79.5	9.5	359	ATPA_BOVIN	P19482 bos taurus

34	79.5	9.5	543	1	ATPA_RAT	P15999 rattus norv
35	79.5	9.5	553	1	ATPA_HUMAN	P25705 homo sapien
36	79.5	9.5	734	1	YKR2_CAEEL	P34308 caenorhabdi
37	79	9.4	593	1	KICJ_HUMAN	P13645 homo sapien
38	78.5	9.4	553	1	ATP0_BOVIN	P19483 bos taurus
39	78.5	9.4	553	1	ATPA_MOUSE	O03265 mus musculu
40	78	9.3	865	1	VGLB_HSYMD	P18538 marek's dis
41	77.5	9.3	219	1	YIAD_ECOLI	P37665 escherichia
42	77	9.2	269	1	CANS_MOUSE	O88456 mus musculu
43	77	9.2	393	1	CSP_PLABR	P14593 plasmodium
44	77	9.2	429	1	CSP_PLAMA	P13815 plasmodium
45	77	9.2	506	1	ATPA_ANASP	P12405 anabaena sp

## ALIGNMENTS

RESULT 1	ID	17KD_RICPR	STANDARD:	PRT:	159 AA.	
AC	P16624:					
DT	01-AUG-1990 (Rel. 15, Created)					
DT	01-AUG-1991 (Rel. 19, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	17 kDa surface antigen precursor.					
GN	OMP OR RP833.					
OS	Rickettsia prowazekii.					
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;					
OC	Rickettsiaceae; Rickettsiae; Rickettsia.					
OX	NCBI_TaxId=782;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Madrid E;					
RC	MEDLINE=89359171; PubMed=2768201;					
RX	MEDLINE=89359171; PubMed=2768201;					
RA	Anderson B.E., Tzianabos T.;					
RT	"Comparative sequence analysis of a genus-common rickettsial antigen					
RT	gene.";					
RL	J. Bacteriol. 171:5199-5201(1989).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Madrid E;					
RC	MEDLINE=99039499; PubMed=9823893;					
RA	Andersson S.G.E., Zomorodipour A., Andersson J.O.,					
RA	Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,					
RT	Eriksson A.-S., Winkler H.H., Kurland C.G.;					
RT	"The genome sequence of Rickettsia prowazekii and the origin of					
RT	mitochondria.";					
RL	Nature 396:133-140(1998).					
CC	-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid					
CC	anchor (Probable).					
CC	-----					
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).					
CC	-----					
DR	EMBL; M28482; AAA26378.1; ALT_SEQ.					
DR	EMBL; AJ235273; CAAL5258.1; -.					
DR	PIR; D33971; D33971.					
DR	PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.					
KW	Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.					
FT	SIGNAL	1	19			
FT	CHAIN	20	159			
FT	LIPID	20	20			
SO	SEQUENCE	159 AA; 16672 MW; A33D404B65EEB071 CRC64;				
Query Match	35.4%;	Score 296;	DB 1;	Length 159;		
Best Local Similarity	38.1%;	Pred. No. 7.1e-19;				
Matches	61;	Conservative	30;	Mismatches	55;	
			Indels	14;	Gaps	4;

QY 9 SLLIIISV---ELVGC--AQNFSRQEVCAIGAVVGGVAGQLPEKGGKRAAMAGCAVIG 63  
Db 5 SKIITIALAASMLQAQNGSGMKNQGTGLTIGGAGGALLGSGFGGKGGLGVGVGALLG 64  
QY 64 GLISKIKGSDMDODK----IKLNGSLKLVYAGQVTRRNRNDTNGSSVLPVATYQRYNK 11  
Db 65 AVLGQIGAGSMDEQDRRLLELTISQRALESAPGSNIIEWRNPDNMGHYVTPNPTY----- 11  
QY 120 QERRQOYCRFEFOOKAMIAAGOKOIEYTCGRPDGQWQYIS 159  
Db 120 RNSAGQYCRREYTOVTIIGKQOKTIGNACRQPDGQWQVYN 159

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RESULT 2
17KD_RICUA
ID 17KD_RICUA STANDARD; PRT; 159 AA.
AC Q52764;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 17 kDa surface antigen precursor.
GN OMP.
OS Rickettsia japonica.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=35790;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YH.
RX MEDLINE=95229950; PubMed=7714214;
RA Furuya Y., Katayama T., Yoshida Y., Kaiho I.;
RT "Specific amplification of Rickettsia japonica DNA from clinical
RT specimens by PCR.";
RL J. Clin. Microbiol. 33:487-489(1995).
CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor (Probable).
-----
CC CC
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-----
CC CC
CC EMBL; D16515; BAA03965.1; -.
DR PROSITE: PS00013; PROKAR.LIPOPROTEIN; 1.
DR outer membrane; Lipoprotein; Antigen; Signal.
FT SIGNAL 1 19
FT CHAIN 20 159 17 KDA SURFACE ANTIGEN.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
SQ SEQUENCE 159 AA; 16554 MW; CDDCE7CEBDDCDBA1 CRC64;
-----
Query Match 35.28; Score 294; DB 1; Length 159;
Best Local Similarity 38.18; Pred. No. 1.le-18;
Matches 61; Conservative 30; Mismatches 55; Indels 14; Gaps 4;
QY 9 SSLIIISV---FLVGC--AQNFSROEYGAATGAUVGVAGGLPEKSGRGVAMATGATLG 63
DB 5 SKIMITIALATSMLOACNPGPMKOGTGITLLGAGGALGSPFGKSGQLGVGVGALLG 64
QY 64 GLIGSKIGSGMOQDQ---IKLNSLEKYKAGGVTFWRNPDNTSNYSVEPRTYQRYNK 119
DB 65 AVLGGOIGAAMDQDRRLAETLSQRALETPAPSGSNVEMRNDNNGYVYPNKTY----- 119
QY 120 QERRROOYCFEFOQKAMTAGOKOELTYGTACGQPPDGRKWOYIS 159
DB 120 RNSTGOTCFREYTGTVVIGKQOKAKAYGNACRPDQMOVYN 159

RESULT 3
17KD_RICCN
ID 17KD_RICCN STANDARD; PRT; 159 AA.

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AC	P05372.1	1988	(Rel. 09, Created)
DT	01-AUG-1990	(Rel. 15, Last sequence update)	
DE	15-JUN-2002	(Rel. 41, Last annotation update)	
OS	17 kDa surface antigen precursor.		
ON	OMP OR RC1287.		
OC	Rickettsia conorii, and		
OC	Rickettsia rickettsii.		
OC	Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;		
OC	Rickettsiaceae; Rickettsiinae; Rickettsia.		
OX	NCBI_TaxId=781, 783;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=R.conorii, and R.rickettsii;		
RX	MEDLINE=89359171; PubMed=2768201;		
RA	Anderson B.E., Tzianabos T.;		
RT	"Comparative sequence analysis of a genus-common rickettsial antigen		
RL	gene.";		
RL	J. Bacteriol. 171:5199-5201(1989).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=R.conorii; STRAIN=Malish 7;		
RX	MEDLINE=21442074; PubMed=1157893;		
RA	Ogata H., Audic S., Renesto-Audiffren P., Fournier P.E., Barbe V.,		
RA	Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,		
RA	Raoult D.;		
RT	"Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";		
RL	Science 293:2093-2098(2001).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=R.rickettsii;		
RA	MEDLINE=87222152; PubMed=3108232;		
RA	Anderson B.E., Regnery R.L., Carbone G.M., Tzianabos T., Mcade J.E.,		
RA	Fu Z.Y., Bellini W.J.;		
RT	"Sequence analysis of the 17-kilodalton-antigen gene from Rickettsia		
RL	J. Bacteriol. 169:2385-2390(1987).		
RN	[4]		
RP	SEQUENCE OF 1-30 FROM N.A.		
RC	SPECIES=R.rickettsii;		
RA	MEDLINE=89008059; PubMed=3139629;		
RA	Anderson B.E., Baumstark B.R., Bellini W.J.;		
RT	"Expression of the gene encoding the 17-kilodalton antigen from		
RT	Rickettsia rickettsii: transcription and posttranslational		
RT	modification.";		
RL	J. Bacteriol. 170:4493-4500(1988).		
CC	-1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid		
CC	anchor (Probable).		
CC	-----		
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CC	-----		
DR	EMBL; M28479; AAA26379.1; -;		
DR	EMBL; M28480; AAA26376.1; -;		
DR	EMBL; AE008675; AAL03825.1; -;		
DR	EMBL; M16486; AAA26381.1; -;		
DR	EMBL; J03371; -; NOT_ANNOTATED_CDS.		
DR	PIR; A25972; A25972.		
DR	PIR; A31836; A31836.		
DR	PIR; A33971; A33971.		
DR	PIR; B33971; B33971.		
DR	PROSITE; PS00013; PROKAR_LIPOPROTEIN_1.		
FW	Outer membrane; Lipoprotein; Antigen; Signal; Complete proteome.		
FT	CHAIN	1	19
FT	SIGNAL	1	19
FT	CHAIN	20	159
FT	LIPID	20	20
FT	CONFLICT	146	146
FT	CONFLICT	153	153
			G -> E (in ref. 3).
			N -> D (in ref. 3).
			N-ACYL DIGLYCERIDE (PROBABLE).





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RESULT 9
17KD_RICMO STANDARD: PRT: 154 AA.
AC P50929:
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 17 kDa surface antigen precursor (Fragment).
GN OMP.
OS Rickettsia montana.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=33991;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ohio 83-441;
RA Stochastic D.R., Ralph D.A., Clark J.B., Fuerst P.A., Pretzman C.;
RL Submitted (Dec-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor (Probable).
-----
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-----
CC
CC EMBL: U1017; AB07705.1;
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Outer membrane; Lipoprotein; Antigen; Signal.
FT SIGNAL 1 BY SIMILARITY.
FT CHAIN 20 >154 17 KDA SURFACE ANTIGEN.
FT LIPID 20 20 N-ACYL DIGLYCERIDE (PROBABLE).
FT NON_TER 154 154
SQ SEQUENCE 154 AA: A09C53B8769E31DA CRC64:
-----
Query Match 30.9%; Score 258; DB 1; Length 154;
Best Local Similarity 36.1%; Pred. No. 1.3e-15;
Matches 56; Conservative 28; Mismatches 57; Indels 14; Gaps 4:
OY 9 SLLIIVV---FLVGC--AQNFSROEVGATGAVGVAGOLFQKSGRVAMAGVAVG 63
DB 5 SKIMTIALASMLQACNGSGMKNKQGTLLGAGGALLGSGFGQKGGVLGVGVALLG 64
OY 64 GLIGSKTGSMMQDQK-----IKLNSLEKVKAGQVTRMRNPDTGNSYVEPVRTYORNK 119
DB 65 AVLGGQIGAGMDEQDRRLAELTSPALSTAPSGSNVEMRNPNGNYGVTPPKTY----- 119
OY 120 QERRPOYCREFOOKAMIAKOKEIVCTACROPDGR 154
DB 120 RSTGQYCREYQTYGVYVIGSKQOKATGNACLOPDDG 154
-----
RESULT 10
17KD_RICCA STANDARD: PRT: 80 AA.
AC P29637:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 17 kDa surface antigen (Fragment).
GN OMP.
OS Rickettsia canada.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=788;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=92108069; PubMed=1729713;
RX

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RA Azad A.F., Sacchi J.B. Jr., Nelson W.M., Dasch G.A.,
RA Schmidtmann E.T., Carl M.;
RT "Genetic characterization and transovarial transmission of a
RT typhus-like rickettsia found in cat fleas.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:43-46(1992).
CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor (Probable).
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-----
CC
CC EMBL: M82879; -; NOT ANNOTATED. CDS.
DR InterPro: IPR000437; PROK_LIPOPROT.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; PARTIAL.
KW Outer membrane; Lipoprotein; Antigen.
FT NON_TER 1 1
FT NON_TER 80 80
SQ SEQUENCE 80 AA: 8372 MW: AD289A48EAB19E0E CRC64:
-----
Query Match 18.8%; Score 157; DB 1; Length 80;
Best Local Similarity 40.3%; Pred. No. 3.5e-07;
Matches 31; Conservative 15; Mismatches 27; Indels 4; Gaps 1:
OY 43 GOLFGSGRVAMAGVAVLGSLGSKIGQSMQDQK-----IKLNSLEKVKAGQVTRMR 98
DB 1 GQFQFGKQGLGVGAGALLGNIQIGAGMDEQDRRLAELTSPALSTAPSGTSTIEMR 60
OY 99 NPDGTGNSYVEPVRTYQ 115
DB 61 NPDNGYGVTPSKTYK 77
-----
RESULT 11
PCP_YEREN STANDARD: PRT: 155 AA.
ID PCP_YEREN
AC P31484:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Outer membrane lipoprotein pcv precursor.
GN PCP OR PCPY.
OS Yersinia enterocolitica.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersiniaceae.
OX NCBI_TaxID=630;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 51872 / WA-C / Serotype O:8;
RX MEDLINE=92121089; PubMed=1732192;
RA Baewmiller A.J., Hantke K.;
RT "A lipoprotein of Yersinia enterocolitica facilitates ferrioxamine
RT uptake in Escherichia coli.";
RL J. Bacteriol. 174:1029-1035(1992).
CC -1- FUNCTION: FACILITATES FERROXAMINE UPTAKE.
CC -1- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor.
CC -1- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLVB AND TO
CC H.INFLUENZAE PCP.
-----
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-----
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CC EMBL: X60448; CAA42977.1; -

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DR PIR: S23787; S23787.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Outer membrane; Lipoprotein; Signal.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 155 OUTER MEMBRANE LIPOPROTEIN PCP.
FT LIPID 18 18 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 155 AA; 15362 MW; 8AD6BE2132E849FA CRC64;

Query Match
Best Local Similarity 24.7%; Pred. No. 0.0038;
Matches 37; Conservative 19; Mismatches 43; Indels 51; Gaps 4;

OY 10 SLIISVFLVGAQN-----FSRQE-----VGAAAT 34
DB 7 AVAIAVATLTCGANNNTLSGDVFSAQAQVOTVYTGILLVSRPYTIGGDDNNVMAIG 66
OY 35 GAVGVGAQVLGKSGGRVAMAIGAVIGLLGSKRIGOSMDQDKIKL----- 82
DB 67 GAVLGGEFNTVGGGTGRSLATPAAGAVAGMAGGVGOGVAMNRTDGVLEVRKDDGTILV 126

OY 83 --NQSEKVKAGQVTRWRNPDIGNSYSVEP 110
DB 127 VOKQGPTRFVSQV--RVMLASSGSTVTYSP 154

RESULT 12
SLYB_ECOLI STANDARD; PRT; 155 AA.
ID SLYB_ECOLI STANDARD; PRT; 155 AA.
AC P55741; P76183;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane lipoprotein slyb precursor.
DE SLYB OR B1641 OR 22655 OR ECS2350.
OS Escherichia coli, and
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=96133688; PubMed=8544813;
RA Ludwig A., Tengell C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,
RT Goebel W.;
RA "SlyA, a regulatory protein from Salmonella typhimurium, induces a
RL hemolytic and pore-forming protein in Escherichia coli.";
RL Mol. Genet. 249:474-486(1995).
RN (2)
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Batliner F.R., Plunkett G. III, Glasner J.D., Rode C.K., Mayhew G.F.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN (3)
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RA MEDLINE=9725157; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakado S., Nakamura Y., Nishimoto H., Nishio Y.,
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubram S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horinouchi T.;
RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN (4)
RP SEQUENCE FROM N.A.

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RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller B.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimailanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatner F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN (5)
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RA MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -i- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
CC anchor (potential).
CC -i- SIMILARITY: TO S.TYPHIMURIUM SLYB, H.INFLUENZAE PCP AND
CC Y. ENTEROCOLITICA PCP.
CC
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CC
CC EMBL, AE000259; AAC74713.1; -
DR EMBL, D90807; BA15402.1; -
DR EMBL, AE005387; AAG56630.1; -
DR EMBL, AP002558; BAB35773.1; -
DR Ecogene: EG13409; SLYB.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
DR Outer membrane; Lipoprotein; Signal; Complete proteome.
KW SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 155 OUTER MEMBRANE LIPOPROTEIN SLYB.
FT LIPID 18 18 N-ACYL DIGLYCERIDE.
FT CONFLICT 98 98 A->T (IN REF. 2).
SQ SEQUENCE 155 AA; 15602 MW; 543EB8A4069A5FA3 CRC64;

Query Match
Best Local Similarity 12.6%; Score 105.5; DB 1; Length 155;
Matches 33; Conservative 21; Mismatches 42; Indels 49; Gaps 4;

OY 13 IISVFLVGAQN-----FSRQE-----VGAAATGAV 37
DB 10 MWGLSLVGGVNDTLSDGYTASEAKQVQNSYGTIVNRPVQIGGDSNVIGAGAV 69
OY 38 VGVGAQVLGKSGGRVAMAIGAVIGLLGSKRIGOSMDQDKIKLNSLEKKAQVTRW 97
DB 70 LGGFLGNTVGGGTGRSLATPAAGAVAGVAGVOSAMNKTGVLEL--ELRK----- 118
OY 98 RNPDTGNSYSVEPRTYRYNKOER 122
DB 119 --DGGNTIIVVOKQGNTRFSPGQR 140

RESULT 13
SLYB_SALTY STANDARD; PRT; 155 AA.
ID SLYB_SALTY STANDARD; PRT; 155 AA.
AC Q53549;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Outer membrane lipoprotein slyb precursor.
RN (4)
RP SEQUENCE FROM N.A.

```

OS *Salmonella typhimurium*, and  
OS *Salmonella typhi*.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC *Salmonella*.  
OX NCBI\_TaxId=602, 601;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhimurium;  
RX MEDLINE=96133688; PubMed=8544813;  
RA Ludwig A., Tengell C., Bauer S., Bubert A., Benz R., Mollenkopf H.-J.,  
RA Goebel W.;  
RT "SlyA, a regulatory protein from *Salmonella typhimurium*, induces a  
haemolytic and pore-forming protein in *Escherichia coli*.";  
RL Mol. Gen. Genet. 249:474-486(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of *Salmonella enterica* serovar *Typhimurium*  
LT2.";  
RL Nature 413:852-856(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhi; STRAIN=CT18;  
RX MEDLINE=21534947; PubMed=11677608;  
RA Parikh H.J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,  
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,  
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
RA Krogan A., Larsen T.S., Leather S., Moulé S., O'Gaora P., Parry C.,  
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
RA Whitehead S., Barrett B.G.;  
RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
enterica serovar *Typhi* CT18.";  
RL Nature 413:848-853(2001).  
RN [4]  
RP SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid  
anchor (Potential).  
CC -1- SIMILARITY: TO E.COLI SLVB, H.INFLUENZAE PCP AND Y. ENTEROCOLITICA  
PCP.  
CC  
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CC  
CC EMBL: S80790; AAB35871.2; -  
DR EMBL: AEO08762; AAL20367.1; -  
DR EMBL: AL627271; CAD01922.1; -  
DR StGene: SG10573; slvB.  
DR PROSITE: PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Outer membrane; Lipoprotein; Signal; Complete proteome.  
FT STGNAL 1 17 POTENTIAL.  
FT CHAIN 18 155 OUTER MEMBRANE LIPOPROTEIN SLVB.  
FT LIPID 18 18 N-ACYL DIGLYCERIDE.  
SQ SEQUENCE 155 AA: 15548 MW: 82FDCCCBABD55A7 CRC64;  
Query Match 12.6%; Score 105.5; DB 1; Length 155;  
Best Local Similarity 24.6%; Pred. No. 0.019; Mismatches 33; Gaps 3;  
Matches 34; Conservative 19; Indels 33; Gaps 3;  
OY 4 GCGGSSLS-----IIISVFLVGCAGNFRNQEVGAATGAVVGAVG 44  
DB 17 GCYVNDSSLSGDVYTTASEAKOVYNTVGTIVNRPVQIQGGSDNSDVGATGAVLGGFLGN 76

OY 45 LFGKSGRVAMAIGAVLGLISKGISQSDQDKIKLNSLEKRVAGOVYTRMRNPDTCN 104  
DB 77 TIGGTGTRSLATAGAVAGVAGVGSAMNKTGVGL--EIKR-----DDGN 122  
OY 105 SYSEVPRTYQRYNRKQER 122  
DB 123 TIMVYOKGNTFRSAGOR 140  
RESULT 14  
PCP\_HAEIN  
ID PCP\_HAEIN STANDARD; PRT; 155 AA.  
AC P10325;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Outer membrane lipoprotein PCP precursor (15 kDa lipoprotein) (PAL  
cross-reacting lipoprotein).  
GN PCP OR LPP OR H1579.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OX NCBI\_TaxId=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88115138; PubMed=2828309;  
RA Delch R.A., Metcalf B.J., Finn C.W., Farley J.E., Green B.A.;  
RT "Cloning of genes encoding a 15,000-dalton peptidoglycan-associated  
outer membrane lipoprotein and an antigenically related 15,000-dalton  
protein from *Haemophilus influenzae*.";  
RL J. Bacteriol. 170:489-498(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Rd / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fieschmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Cocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Ullrich D.T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georgagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of *Haemophilus influenzae*  
Rd.";  
RL Science 269:496-512(1995).  
RN [3]  
RP SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid  
anchor.  
CC -1- SIMILARITY: TO E.COLI AND S.TYPHIMURIUM SLVB AND TO  
Y. ENTEROCOLITICA PCP.  
CC  
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CC  
CC EMBL: M18877; AAA24938.1; -  
DR EMBL: U32832; AAC23228.1; -  
DR PIR: B28543; B28543.  
DR TIGR: H11579; -  
DR PROSITE: PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Outer membrane; Lipoprotein; Signal; Complete proteome.  
FT STGNAL 1 18  
FT CHAIN 19 155 OUTER MEMBRANE LIPOPROTEIN PCP.  
FT LIPID 19 19 N-ACYL DIGLYCERIDE.  
FT CONFLICT 135 143 CSUVAEFPV--> VAGRVRI (IN REF. 1).  
SQ SEQUENCE 155 AA: 15425 MW: D7880327FEC0C985 CRC64;  
Query Match 12.2%; Score 102; DB 1; Length 155;

Best Local Similarity 39.6%; Pred. No. 0.038;  
Matches 21; Conservative 9; Mismatches 23; Indels 0; Gaps 0;

OY 30 VGATGAVGVAGOLFPGKSGRVAMAIGAVLGLISKGISMDQDQKIL 82  
11 : 11:11 11:11 : 11:11:1111:11:11 : 11  
DB 62 VGLGGGALGGAGSTIGGGRGOAIAVGAIGAGTASKEKMSQVNGAEI 114

## RESULT 15

YCFJ\_ECOLI STANDARD: PRT; 179 AA.  
ID YCFJ\_ECOLI  
AC P37996; P75951;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical protein ycfJ.  
GN YCFJ OR B1110.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426517; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RL "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97061202; PubMed=8905232;  
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
RA Yano M., Horiuchi T.;  
RL "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 12-7-28.0 min region on the linkage map.";  
RL DNA Res. 3:137-155(1996).  
RN [3]  
RP SEQUENCE OF 1-63 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=81236546; PubMed=6265208;  
RA Young J.G., Rogers B.L., Campbell H.D., Jaworski A., Shaw D.C.;  
RL "Nucleotide sequence coding for the respiratory NADH dehydrogenase of  
Escherichia coli. UUG initiation codon.";  
RL Eur. J. Biochem. 116:165-170(1981).  
RN [4]  
RP IDENTIFICATION.  
RX MEDLINE=95075659; PubMed=7984428;  
RA Borodovsky M., Rudd K.E., Koonin E.V.;  
RL "Intrinsic and extrinsic approaches for detecting genes in a  
bacterial genome.";  
RL Nucleic Acids Res. 22:4756-4767(1994).  
CC -I- SIMILARITY: TO RICKETTSIA 17 KDa SURFACE ANTIGEN.  
CC -----  
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CC -----  
CC EMBL: AE000211; AAC7A194.1;  
DR EMBL: D90746; BAA35925.1;  
DR EMBL: V00306; NOT\_ANNOTATED\_CDS.  
DR ECGene: EG12444; ycfJ.

KW Hypothetical protein: Transmembrane: Complete proteome.  
FT TRANSMEM 25 POTENTIAL.  
SQ SEQUENCE 179 AA; 18920 MW; BA5EB0DB56D45609 CRC64;

Query Match 11.8%; Score 99; DB 1; Length 179;  
Best Local Similarity 27.1%; Pred. No. 0.079;  
Matches 26; Conservative 12; Mismatches 32; Indels 26; Gaps 1;

OY 31 GAATGAVGVAGOLFPGKSGRVAMAIGAVLGLISKGISMDQDQKILNQSLKVK 90  
11 : 11:11 11:11 : 11:11:1111:11:11 : 11  
DB 73 GSVLGAVAGVIGHQFPGGGRGDVATVWGAALGGYAGNIOGSLQESD----- 120  
OY 91 AGQVTRMRNPDTGNSYSVEPVRTQRYNKOERROQY 126  
11 : 11:11 11:11 : 11:11:1111:11:11 : 11  
DB 121 -----TITTTQORCKTVYDKSEKMLGY 142

Search completed: February 12, 2003, 16:44:11  
Job time : 52 secs









A:Molecule type: DNA  
 A:Residues: 1-155 <BAE>  
 A:Cross-references: EMBL:X60448; NID:948577; PIDN:CAA42977.1; PID:948579  
 C:Superfamily: PAL cross-reacting lipoprotein

Query Match 13.6%; Score 113.5; DB 2; Length 155;  
 Best Local Similarity 24.7%; Pred. No. 0.007;  
 Matches 37; Conservative 19; Mismatches 43; Indels 51; Gaps 4;

QY 10 SLTIISVFLVGAQN-----FSRQE-----VGAT 34  
 DB 7 AVALAVLTTCGANNNTLSGVDFSSAQKQVTVYTGTLISVPVLTGGDDNNVMGAIG 66  
 QY 35 GAVVGAVAGOLFPGKSGRVAMAGVAGLIGSKIGSQMPQODKIKL----- 82  
 DB 67 GAVLGGFLGNFVGGGTGSLATAGAVAGMAGCGVCGAMRTDGVLEVRKDDGTTILV 126  
 QY 83 --NQSLEVKVKAQVTRWRNPDTGNSYSEP 110  
 DB 127 VOKGPTREVSQG--RVMLASSGTIVSP 154

RESULT 11  
 B82837  
 Conserved hypothetical protein XP0178 [imported] - Xylella fastidiosa (strain 9a5c)  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: B82837

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: B82837

A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-257 <SIM>  
 A:Cross-references: GB:AE003872; GB:AE003849; NID:9104975; PIDN:AAF82991.1; GSPDB:GN001

A:Experimental source: strain 9a5c  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvaeng, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H  
 as-Melo, E.; Docena, C.; El-Dorry, H.; Facinca, A.P.; Ferreira, A.J.S.  
 Submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kikajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
 Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F  
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
 M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:

A:Gene: XP0178

Query Match 13.4%; Score 112; DB 2; Length 257;  
 Best Local Similarity 50.0%; Pred. No. 0.016;

Matches 20; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 31 GAATGAVGAVAGOLFPGKSGRVAMAGVAGLIGLSK 70  
 DB 105 GTAIGALIGLVGNORGHNGRKALTAAGAVAGGTIGNEV 144

RESULT 12

AD2696

lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002

C:Accession: AD2696

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam  
 ster, E.W.

A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; PMID:11743193

A:Accession: AD2696

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-142 <KUR>  
 A:Cross-references: GB:AE008688; PIDN:AAL41986.1; PID:917739358; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: lipA

A:Map position: circular chromosome

Query Match 13.3%; Score 111.5; DB 2; Length 142;  
 Best Local Similarity 27.2%; Pred. No. 0.0096;  
 Matches 41; Conservative 21; Mismatches 60; Indels 29; Gaps 9;

QY 10 SLTIISVFLVGAQNFSRQEVGAATGAVVGAVAGOLFPGKSGRVAMAGVAGLIGLSK 69  
 DB 12 SILCVSW-LSAC-----TTGTRPAG--GSLFGR-SAQSPPLANIGGIVG-K 56  
 QY 70 IGSMQODKIKL-----NQSLEVKVKAQVTRWRNPDT-GNSYSEVRYTORNKOERQ 124  
 DB 57 SGVELDGDGTALAEVYKALETAPVGTPIYMTGDDVKQGVANAP---YQGN----- 107

QY 125 QYCEFFQKAMIAQKQEIYGTAROPDGRW 155  
 DB 108 QNCROYSHLITVDGRTRVRGAACRNDGWSW 138

RESULT 13  
 D97478

lipA protein [imported] - Agrobacterium tumefaciens (strain C58, Cereon)  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002

C:Accession: D97478

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm  
 A.; Liu, F.; Woliam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz,  
 Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium  
 A:Reference number: A97359; PMID:11743194

A:Accession: D97478

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-125 <KOR>  
 A:Cross-references: GB:AE007869; PIDN:AAK86781.1; PID:915155981; GSPDB:GN00169

C:Genetics:

A:Gene: AGR C.1782

A:Map position: circular chromosome

Query Match 13.3%; Score 111; DB 2; Length 125;  
 Best Local Similarity 27.5%; Pred. No. 0.0093;  
 Matches 36; Conservative 18; Mismatches 61; Indels 16; Gaps 6;

QY 30 VCAATGAVGAVAGOLFPGKSGRVAMAGVAGLIGLSKIGSQSDQDKIKL-----NQS 85  
 DB 2 LSACTTTGTRPAGSLFGR-SAQSPPLANIGGIVG-KSGVELDRDQTKALEAEYKA 59  
 QY 86 LEKRVAGVTRWRNPDT-GNSYSEVRYTORNKOERQYCEFFQKAMIAQKQEIY 144  
 DB 60 LETAPVGTPIYMTGDDVKQGVANAP---YQGN-----QNCROYSHLITVDGRTRVR 110  
 QY 145 GTACRQPDGRW 155  
 DB 111 GAACRNDGWSW 121

RESULT 14

S58234  
 lipA protein - Rhizobium leguminosarum

C:Species: Rhizobium leguminosarum  
C:Date: 13-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 08-Oct-1999  
C:Accession: S58234  
R:Yeoman, K.H.; Delgado, M.J.; Downie, J.A.; Johnston, A.W.B.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: S58232

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OM protein - protein search, using sw model

Run on: February 12, 2003, 16:34:58 : Search time 36 Seconds  
(without alignments)  
599.628 Million cell updates/sec

Title: US-09-677-374-2

Perfect score: 836  
1 MNRCLGSLIITVFLV.....ITYGACRQPDGRWQVISTEK 162

Sequence:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Scoring table:

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:

908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	836	100.0	162	22	AAAG78025
2	836	100.0	162	23	AAAB81126
3	836	100.0	162	23	AAU97867
4	815	97.5	161	22	AAAB81127
5	815	97.5	161	23	AAU97868
6	815	97.5	256	22	AAAB81128
7	815	97.5	256	23	AAU97869
8	112	13.4	20	22	AAAB81130
9	112	13.4	20	23	AAU97871
10	108	12.9	197	23	AA017565

11	108	12.9	224	22	AAAB20105
12	105.5	12.6	223	20	AAV34487
13	105.5	12.6	230	20	AAV34362
14	102	12.2	154	11	AAAR05799
15	98	11.7	309	22	ABG15906
16	91	10.9	528	22	AAAB82611
17	86.5	10.3	2309	22	ABBB6232
18	82	9.8	666	22	ABBS6019
19	81.5	9.7	651	20	AAV40097
20	81.5	9.7	651	23	AAU17781
21	81.5	9.7	718	12	AAAR14308
22	81.5	9.7	718	19	AAAW53346
23	81.5	9.7	718	21	AAV59070
24	80.5	9.6	102	22	AAAM1943
25	80.5	9.6	170	22	ABP37981
26	80.5	9.6	302	22	AAAM40157
27	80.5	9.6	302	23	AAU74394
28	80.5	9.6	318	22	ABP37982
29	80.5	9.6	542	22	ABBB65790
30	80.5	9.6	542	22	ABBB65791
31	80.5	9.6	542	22	ABBB70501
32	80.5	9.6	1640	23	ABBS4727
33	80	9.6	116	19	AAV11028
34	80	9.6	2017	22	ABG06301
35	80	9.6	2599	21	AAV75098
36	79	9.4	112	23	ABP28121
37	79	9.4	618	21	ABBS6803
38	78.5	9.4	581	23	ABP25639
39	78	9.3	104	23	AAAM50034
40	78	9.3	137	23	AAAM50036
41	78	9.3	219	23	AAAM50040
42	78	9.3	230	23	AAAM50035
43	78	9.3	264	23	AAAM50048
44	78	9.3	271	23	AAAM50044
45	78	9.3	364	23	AAAM50043

#### ALIGNMENTS

RESULT 1	
AAAG78025	standard; Protein: 162 AA.
AC	AAAG78025;
DT	15-JAN-2002 (first entry)
DE	Piscirickettsia salmonis polypeptide P10.6.
XX	
KW	Piscirickettsia salmonis; Piscirickettsiosis; salmonid rickettsial;
KW	septicemia; SRS; surface antigen; vaccine; antibacterial; fish;
XX	ATCC VR-1361.
XX	
OS	Piscirickettsia salmonis.
XX	
PN	WO200168865-A2.
XX	
PD	20-SEP-2001.
XX	
PF	12-MAR-2001; 2001WO-GB01055.
XX	
PR	11-MAR-2000; 2000GB-0005838.
PR	01-JUL-2000; 2000GB-0016080.
PR	29-JUL-2000; 2000GB-0018599.
XX	
PA	(AQUA-) AQUA HEALTH EURO LTD.
XX	
PI	Simard N, Brouwers H, Jones S, Griffiths S, Valenzuela P;
PI	Burzio L;
XX	
DR	WPI: 2001-639050/73.

Moraxella catarrha  
Porphyromonas ging  
Porphyromonas ging  
POMP-2 gene prod.  
Novel human diagno  
Spider recombinant  
Drosophila melanog  
Drosophila melanog  
Spider silk protein  
Spider natural sil  
N.clavipes draglin  
Nephila clavipes s  
N. clavipes spider  
Human polypeptide  
Human GS930284 pro  
Human polypeptide  
Human ovarian tumo  
Human GS930284 pro  
Drosophila melanog  
Drosophila melanog  
Lactococcus lactis  
H. pylori ORF 01cp  
Novel human diagno  
Streptococcus poly  
Human prostate can  
Streptococcus poly  
N. clavipes spidero  
N. clavipes spidero  
N. clavipes spidero  
N. clavipes spidero  
N. clavipes spidero  
N. clavipes spidero

DR N-PSDB; AAH79040.

XX New nucleic acids encoding an amino acid sequence homologous to the  
PT surface antigen present on *Piscirickettsia salmonis* are useful to  
PT protect fish against *Piscirickettsiosis* -  
XX  
PS Claim 6; Fig 5; 25pp; English.

XX The invention relates to nucleic acid sequences and the encoded protein  
CC of a least part of the surface antigen present on *Piscirickettsia*  
CC salmonis for production of a vaccine with antibacterial activity to  
CC protect fish against *P. salmonis* which causes *Piscirickettsiosis*, also  
CC known as salmonid rickettsial septicemia.  
XX  
SQ Sequence 162 AA:

Query Match 100.0%; Score 836; DB 22; Length 162;  
Best Local Similarity 100.0%; Pred. No. 3.8e-80;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNRGCLQSSSLITISVFLVGCANFNSROEVGAATGAVGVAGQLFGKSGRYAMAIGGA 60
DB 1 MNRGCLQSSSLITISVFLVGCANFNSROEVGAATGAVGVAGQLFGKSGRYAMAIGGA 60
QY 61 VLGLIGSKTIGQSMDOODKIKLNOSLEKVKAGQVTRMRNPDGNSYSVEPRTYORYNKQ 120
DB 61 VLGLIGSKTIGQSMDOODKIKLNOSLEKVKAGQVTRMRNPDGNSYSVEPRTYORYNKQ 120
QY 121 ERROQYCREFOOKAMTAGOKOEIYGTACROPDGRMOWISTEK 162
DB 121 ERROQYCREFOOKAMTAGOKOEIYGTACROPDGRMOWISTEK 162
```

RESULT 2  
AAB81126  
ID AAB81126 standard; Protein; 162 AA.  
XX  
AC AAB81126;  
XX  
DT 11-JUL-2001 (first entry)  
XX  
DE OSPA antigen amino acid sequence.

XX  
KM Poikilothermic fish; *Piscirickettsia salmonis*; rickettsial pathogen;  
KM vaccine; Ospa; salmonid rickettsial septicemia; rickettsial disease;  
XX  
OS *Piscirickettsia salmonis*.

XX Key Location/Qualifiers  
FT 110..129  
XX Region /label=B\_cell\_epitope  
XX  
CA2281913-A1.  
XX  
PD 17-MAR-2001.  
XX  
PF 17-SEP-1999; 99CA-2281913.  
XX  
PR 17-SEP-1999; 99CA-2281913.

XX (KAYW/) KAY W W.  
PA (BURI/) BURIAN J.  
PA (KUZV/) KUZIK M A.  
XX  
PI Kay WW, Burian J, Kuzik MA;  
XX  
DR WPI: 2001-316844/34.  
DR N-PSDB; AAF86246.  
XX  
PT

Method for protecting poikilothermic fish against salmonid rickettsial  
PT septicemia and other rickettsial diseases comprises administering a  
XX vaccine containing the Ospa protein of *Piscirickettsia salmonis* -

XX Example 2; Fig 2B; 35pp; English.  
PS  
XX  
XX

CC This invention relates to a method for the protection against infection  
CC of a poikilothermic fish by the bacterial pathogen, *Piscirickettsia*  
CC salmonis. The method comprises administering an immunogenic amount of a  
CC *P. salmonis* specific antigen termed Ospa, or an immunogenic fragment of a  
CC Ospa in the form of a vaccine. The method is used for protecting animals,  
CC particularly poikilothermic fish, against the bacterial pathogen  
CC *P. salmonis*. The method is also useful for protecting against salmonid  
CC rickettsial septicemia (SRS) and other rickettsial diseases. The present  
CC sequence represents *P. salmonis* Ospa protein. An Ospa protein with an  
CC N-terminal fusion partner is used in a vaccine to create an anti-Ospa  
XX antibody response.  
XX  
SQ Sequence 162 AA:

Query Match 100.0%; Score 836; DB 22; Length 162;  
Best Local Similarity 100.0%; Pred. No. 3.8e-80;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MNRGCLQSSSLITISVFLVGCANFNSROEVGAATGAVGVAGQLFGKSGRYAMAIGGA 60
DB 1 MNRGCLQSSSLITISVFLVGCANFNSROEVGAATGAVGVAGQLFGKSGRYAMAIGGA 60
QY 61 VLGLIGSKTIGQSMDOODKIKLNOSLEKVKAGQVTRMRNPDGNSYSVEPRTYORYNKQ 120
DB 61 VLGLIGSKTIGQSMDOODKIKLNOSLEKVKAGQVTRMRNPDGNSYSVEPRTYORYNKQ 120
QY 121 ERROQYCREFOOKAMTAGOKOEIYGTACROPDGRMOWISTEK 162
DB 121 ERROQYCREFOOKAMTAGOKOEIYGTACROPDGRMOWISTEK 162
```

RESULT 3  
AAU97867  
ID AAU97867 standard; Protein; 162 AA.  
XX  
AC AAU97867;  
XX  
DT 12-AUG-2002 (first entry)  
XX  
DE *Piscirickettsia salmonis* outer surface lipoprotein Ospa.

XX  
KM Outer surface lipoprotein; Ospa; antibacterial; immunosuppressive;  
KM vaccine; poikilothermic fish; fin-fish; Rickettsial septicemia;  
XX  
OS *Piscirickettsia salmonis*.

XX Key Location/Qualifiers  
FT 110..129  
XX Region /label=B\_cell\_epitope  
XX  
CA2339327-A1.  
XX  
PD 15-MAR-2002.  
XX  
PF 19-MAR-2001; 2001CA-2339327.  
XX  
PR 15-SEP-2000; 2000US-0677374.

XX (THOR/) THORNTON J C.  
PA (KAYW/) KAY W W.  
PA (BURI/) BURIAN J.  
PA (KUZV/) KUZIK M A.  
XX  
PI Thornton JC, Kay WW, Burian J, Kuzik MA;  
XX  
DR WPI: 2002-455221/49.  
DR N-PSDB; ABK52401.  
XX  
PT

Inducing immunity in fin fish to Rickettsial septicemia, comprises  
PT administration of an outer surface lipoprotein (Ospa) of a bacterial  
XX strain, as a vaccine -  
XX  
XX Claim 15; Fig 2; 55pp; English.



```

XX CC The invention describes a method of protecting a poikilothermic fish
XX CC against infection by the bacterial pathogen Piscirickettsia salmonis
XX CC comprising administering either intraperitoneally, by immersion or
XX CC orally, an immunogenic amount of principal antigen, the Ospa (outer
XX CC surface lipoprotein), its variants, non-lipidated form or antigenic
XX CC peptides derived or synthesized with or without an adjuvant. The new
XX CC method is used to provide an outer surface lipoprotein (Ospa) of
XX CC bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity
XX CC in fin-fish against Rickettsial septicaemia and other related
XX CC Rickettsial diseases caused by either a virus, bacteria or parasite.
XX CC This is the amino acid sequence of the Piscirickettsia salmonis outer
XX CC surface lipoprotein, Ospa, used in the creation of the vaccine described
XX CC in the invention.
XX SO Sequence 162 AA:

Query Match          100.0%; Score 836; DB 23; Length 162;
Best Local Similarity 100.0%; Pred. No. 3.8e-80;
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNRGCGSSLIITISVFLVGCANFNRQEVGATGAVGVAGOLFPGSGRVAMAIGA 60
DB 1 MNRGCGSSLIITISVFLVGCANFNRQEVGATGAVGVAGOLFPGSGRVAMAIGA 60
OY 61 VLGGLGSKIGQSMQODKIKLNQSLKVKAGQVTRMRNPDTGNSYVEPVRTYQRYNKO 120
DB 61 VLGGLGSKIGQSMQODKIKLNQSLKVKAGQVTRMRNPDTGNSYVEPVRTYQRYNKO 120
OY 121 ERROQCREFOOKAMIAQOKETIGTACROPDGRMVOYISTEK 162
DB 121 ERROQCREFOOKAMIAQOKETIGTACROPDGRMVOYISTEK 162

RESULT 4
AAB81127
ID AAB81127 standard; Protein: 161 AA.
AC AAB81127;
DT 11-JUL-2001 (first entry)
DE Optimised Ospa protein 17E2 amino acid sequence.
KW Poikilothermic fish; Piscirickettsia salmonis; rickettsial pathogen;
KW vaccine; Ospa; salmonid rickettsial septicaemia; rickettsial disease;
KW SRS.
XX Piscirickettsia salmonis.
XX OS Synthetic.
XX FH Key
XX FT Region Location/Qualifiers
XX FT 109..128 /label=B_cell_1epitope
XX CA2281913-A1.
XX PD 17-MAR-2001.
XX PF 17-SEP-1999; 99CA-2281913.
XX PR 17-SEP-1999; 99CA-2281913.
XX (KAWW/) KAY W W.
XX (BURI/) BURIAN J.
XX (KUYZ/) KUYZK M A.
XX PI Kay WW, Burian J, Kuzyk MA;
XX DR WPI: 2001-316844/34.
XX DR N-PSDB: AAF86247.
XX PT Method for protecting poikilothermic fish against salmonid rickettsial

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PT septicemia and other rickettsial diseases comprises administering a
XX vaccine containing the Ospa protein of Piscirickettsia salmonis
XX PS Disclosure: Fig 5: 35pp: English.
XX CC This invention relates to a method for the protection against infection
XX CC of a poikilothermic fish by the bacterial pathogen, Piscirickettsia
XX CC salmonis. The method comprises administering an immunogenic amount of a
XX CC P. salmonis specific antigen termed Ospa, or an immunogenic fragment of
XX CC Ospa in the form of a vaccine. The method is used for protecting animals,
XX CC particularly poikilothermic fish, against the bacterial pathogen
XX CC P. salmonis. The method is also useful for protecting against salmonid
XX CC rickettsial septicaemia (SRS) and other rickettsial diseases. The present
XX CC sequence represents optimised P. salmonis Ospa protein 17E2. The DNA
XX CC encoding Ospa 17E2 (AA86247) has been optimised for expression in
XX CC Escherichia coli. An Ospa protein with an N-terminal fusion partner is
XX CC used in a vaccine to create an anti-Ospa antibody response.
XX SO Sequence 161 AA:

Query Match          97.5%; Score 815; DB 22; Length 161;
Best Local Similarity 98.8%; Pred. No. 6.2e-78;
Matches 158; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 RCGLOGSSLIITISVFLVGCANFNRQEVGATGAVGVAGOLFPGSGRVAMAIGA 62
DB 2 RCGLOGSSLIITISVFLVGCANFNRQEVGATGAVGVAGOLFPGSGRVAMAIGA 61
OY 63 GGLIGSKIGQSMQODKIKLNQSLKVKAGQVTRMRNPDTGNSYVEPVRTYQRYNKO 122
DB 62 GGLIGSKIGQSMQODKIKLNQSLKVKAGQVTRMRNPDTGNSYVEPVRTYQRYNKO 121
OY 123 RQOYCREFOOKAMIAQOKETIGTACROPDGRMVOYISTEK 162
DB 123 RQOYCREFOOKAMIAQOKETIGTACROPDGRMVOYISTEK 161

RESULT 5
AAU97868
ID AAU97868 standard; Protein: 161 AA.
AC AAU97868;
DT 12-AUG-2002 (first entry)
DE Escherichia coli codon optimised Ospa, 17E2.
XX Escherichia coli codon optimised Ospa, 17E2.
XX KW Outer surface lipoprotein; Ospa; antibacterial; immunosuppressive;
XX KW vaccine; poikilothermic fish; fin-fish; Rickettsial septicaemia;
XX KW Rickettsial disease; 17E2.
XX Piscirickettsia salmonis.
XX OS Synthetic.
XX FH Key
XX FT Region Location/Qualifiers
XX FT CA2339327-A1.
XX PD 15-MAR-2002.
XX PF 19-MAR-2001; 2001CA-2339327.
XX PR 15-SEP-2000; 2000US-0677374.
XX (THOR/) THORNTON J C.
XX (KAWW/) KAY W W.
XX (BURI/) BURIAN J.
XX (KUYZ/) KUYZK M A.
XX PI Thornton JC, Kay WW, Burian J, Kuzyk MA;
XX DR WPI: 2002-455221/49.
XX DR N-PSDB: ABR52402.
XX PT Inducing immunity in fin fish to Rickettsial septicaemia, comprises

```

(KAYW/) KAY W W.  
(BURI/) BURIAN J.

(THOR/) THORNTON J C.  
(KAYH/) KAY C T

PA (KUZT/) KUZTK M A.  
 XX Thornton JC, Kay WW, Burian J, Kuzyk MA;  
 PI WPI; 2002-455221/49.  
 DR N-PSDB; ABR52403.  
 XX  
 PT Inducing immunity in fin fish to Rickettsial septicaemia, comprises  
 PT administration of an outer surface lipoprotein (Osps) of a bacterial  
 PT strain, as a vaccine -  
 XX  
 PS Example 4; Fig 5; 55pp; English.  
 XX  
 CC This invention describes a method of protecting a polkithohermic fish  
 CC against infection by the bacterial pathogen Piscirickettsia salmonis  
 CC comprising administering either intraperitoneally, by immersion or  
 CC orally, an immunogenic amount of principal antigen, the Osps (outer  
 CC surface lipoprotein), its variants, non-lipidated form or antigenic  
 CC peptides derived or synthesized with or without an adjuvant. The new  
 CC method is used to provide an outer surface lipoprotein (Osps) of  
 CC bacterial strain Piscirickettsia salmonis as a vaccine to induce immunity  
 CC in fin-fish against Rickettsial septicaemia and other related  
 CC Rickettsial diseases caused by either a virus, bacteria or parasite.  
 CC This is the amino acid sequence of the Escherichia coli codon optimised  
 CC outer surface lipoprotein Osps (117e2) with an N-terminal fusion used in  
 CC the creation of the vaccine described in the invention.  
 XX  
 SQ Sequence 256 AA;  
 QY Query Match 97.5%; Score 815; DB 23; Length 256;  
 DB Best Local Similarity 98.8%; Pred. No. 1.1e-77;  
 Matches 158; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 OY 3 RCGLOGSSLIITISVPLVGCAGNFSROEVGAATGAVVGVAGVAFGKSGRVAMATGAVL 62  
 DB 97 RCGLOGSSLIITISVPLVGCAGNFSROEVGAATGAVVGVAGVAFGKSGRVAMATGAVL 156  
 OY 63 GGLIGSKTIGSMDQODKIKINOSLEKVKAGQVTRWRNPDTGNSYSVEPVRYORYNKQER 122  
 DB 157 GGLIGSKTIGSMDQODKIKINOSLEKVKAGQVTRWRNPDTGNSYSVEPVRYORYNKQER 216  
 OY 123 ROOYCREFOOKAMIAQOKOEIYGTACROPDGRNOVISTEK 162  
 DB 217 ROOYCREFOOKAMIAQOKOEIYGTACROPDGRNOVISTEK 256  
 RESULT 8  
 AAB81130  
 ID AAB81130 standard; Peptide; 20 AA.  
 XX  
 AC AAB81130;  
 XX  
 DT 11-JUL-2001 (first entry)  
 XX  
 DE Osps B-cell epitope peptide #2.  
 XX  
 KW Polkithohermic fish; Piscirickettsia salmonis; rickettsial pathogen;  
 KW vaccine; Osps; salmonid rickettsial septicaemia; rickettsial disease;  
 KW SRS; antibody.  
 XX  
 OS Piscirickettsia salmonis.  
 XX  
 PN CA2281913-A1.  
 XX  
 PD 17-MAR-2001.  
 XX  
 PF 17-SEP-1999; 99CA-2281913.  
 XX  
 PR 17-SEP-1999; 99CA-2281913.  
 XX  
 PA (KAWW/) KAY W W.  
 PA (BURT/) BURIAN J.  
 PA (KUZT/) KUZTK M A.

XX Kay WW, Burian J, Kuzyk MA;  
 PI WPI; 2001-316844/34.  
 DR  
 XX  
 XX Method for protecting polkithohermic fish against salmonid rickettsial  
 PT septicaemia and other rickettsial diseases comprises administering a  
 PT vaccine containing the Osps protein of Piscirickettsia salmonis -  
 XX  
 PS Example 2; Page 17; 35pp; English.  
 XX  
 CC This invention relates to a method for the protection against infection  
 CC of a polkithohermic fish by the bacterial pathogen, Piscirickettsia  
 CC salmonis. The method comprises administering an immunogenic amount of a  
 CC P. salmonis specific antigen termed Osps, or an immunogenic fragment of  
 CC Osps in the form of a vaccine. The method is used for protecting animals,  
 CC particularly polkithohermic fish, against the bacterial pathogen  
 CC P. salmonis. The method is also useful for protecting against salmonid  
 CC rickettsial septicaemia (SRS) and other rickettsial diseases. The present  
 CC sequence represents an immunogenic epitope of the P. salmonis Osps  
 CC protein. The peptide is used to raise rabbit anti-Osps antibodies.  
 XX  
 SQ Sequence 20 AA;  
 QY Query Match 13.4%; Score 112; DB 22; Length 20;  
 DB Best Local Similarity 100.0%; Pred. No. 5.9e-05;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 110 PVRYTORYNKQERRROOYCRE 129  
 DB 1 PVRYTORYNKQERRROOYCRE 20  
 RESULT 9  
 AA097871  
 ID AA097871 standard; Peptide; 20 AA.  
 XX  
 AC AA097871;  
 XX  
 DT 12-AUG-2002 (first entry)  
 XX  
 DE Outer surface lipoprotein Osps based peptide #2.  
 XX  
 KW Outer surface lipoprotein: Osps; antibacterial; immunosuppressive;  
 KW vaccine; polkithohermic fish; fin-fish; Rickettsial septicaemia;  
 KW Rickettsial disease.  
 XX  
 OS Piscirickettsia salmonis.  
 OS Synthetic.  
 OS  
 PN CA2339327-A1.  
 XX  
 PD 15-MAR-2002.  
 XX  
 PF 19-MAR-2001; 2001CA-2339327.  
 XX  
 PR 15-SEP-2000; 2000US-0677374.  
 XX  
 PA (THOR/) THORNTON J C.  
 PA (KAWW/) KAY W W.  
 PA (BURT/) BURIAN J.  
 PA (KUZT/) KUZTK M A.  
 XX  
 PI Thornton JC, Kay WW, Burian J, Kuzyk MA;  
 XX  
 DR WPI; 2002-455221/49.  
 XX  
 PT Inducing immunity in fin fish to Rickettsial septicaemia, comprises  
 PT administration of an outer surface lipoprotein (Osps) of a bacterial  
 PT strain, as a vaccine -  
 XX  
 PS Example 2; Page 17; 55pp; English.  
 XX

CC The invention describes a method of protecting a poikilothermic fish  
CC against infection by the bacterial pathogen *Piscirickettsia salmonis*  
CC comprising administering either intraperitoneally, by immersion or  
CC orally, an immunogenic amount of principal antigen, the OSPA (outer  
CC surface lipoprotein), its variants, non-lipidated form or antigenic  
CC peptides derived or synthesized with or without an adjuvant. The new  
CC method is used to provide an outer surface lipoprotein (OSPA) of  
CC bacterial strain *Piscirickettsia salmonis* as a vaccine to induce immunity  
CC in fin-fish against *Rickettsial* septicemia and other related  
CC *Rickettsial* diseases caused by either a virus, bacteria or parasite.  
CC This sequence represents a synthetic peptide used to create polyclonal  
CC rabbit antibodies against the *Piscirickettsia salmonis* outer surface  
CC lipoprotein, OSPA.

XX  
XX Sequence 20 AA:

Query Match 13.4%; Score 112; DB 23; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.9e-05;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 PVRTYQRYNKKERRQOYCRE 129

Db 1 PVRTYQRYNKKERRQOYCRE 20

RESULT 10

AA017565  
ID AA017565 standard; Protein; 197 AA.

XX  
XX AA017565;

DT 19-JUL-2002 (first entry)

DE M catarrhalis MCA100414 protein SEQ ID NO: 10.

XX  
XX Moraxella; vaccine; respiratory tract infection; antiinflammatory;

KW auditory; antibacterial; otitis media; sinusitis; pneumonia.

XX  
XX Moraxella catarrhalis.

OS  
PN WO200218595-A2.

XX  
PD 07-MAR-2002.

PF 28-AUG-2001: 2001MO-CA01221.

XX  
PR 28-AUG-2000: 2000US-228294P.

PR 28-AUG-2000: 2000US-228295P.

PR 28-AUG-2000: 2000US-228296P.

PR 29-AUG-2000: 2000US-228438P.

PR 29-AUG-2000: 2000US-228439P.

PR 29-AUG-2000: 2000US-228440P.

PR 29-AUG-2000: 2000US-228441P.

PR 29-AUG-2000: 2000US-228442P.

PR 29-AUG-2000: 2000US-228443P.

PR 29-AUG-2000: 2000US-228511P.

PR 29-AUG-2000: 2000US-228512P.

PR 29-AUG-2000: 2000US-228742P.

PR 29-AUG-2000: 2000US-228773P.

PR 01-SEP-2000: 2000US-229465P.

PR 01-SEP-2000: 2000US-229474P.

PR 01-SEP-2000: 2000US-229475P.

PR 01-SEP-2000: 2000US-229478P.

PR 05-SEP-2000: 2000US-229740P.

PR 05-SEP-2000: 2000US-229803P.

PR 05-SEP-2000: 2000US-229804P.

PR 05-SEP-2000: 2000US-229805P.

PR 05-SEP-2000: 2000US-229806P.

PR 05-SEP-2000: 2000US-229809P.

PR 05-SEP-2000: 2000US-229811P.

PR 06-SEP-2000: 2000US-230214P.

PR 06-SEP-2000: 2000US-230250P.

PR 06-SEP-2000: 2000US-230252P.

XX  
PA (AVET ) AVENTIS PASTEUR LTD.

XX  
PI Loosmore S, Wang J, Bradley B, Ochs M, Yang Y;

XX  
DR WPI; 2002-401721/43.

XX  
DR N-PSDB; AAL46497.

PT Moraxella polypeptide and polynucleotides useful as vaccine for

PT immunizing a host e.g. humans against disease e.g. otitis media,

XX pneumonia, caused by infection of the bacteria

PS Claim 28; Fig 9; 277pp; English.

XX  
XX

CC The present invention provides the protein and coding sequences of  
CC proteins from Moraxella catarrhalis. These can be used to produce  
CC vaccines which protect against M. catarrhalis infection, which can cause  
CC otitis media, respiratory infection, sinusitis, and pneumonia. The  
CC present sequence is a protein of the invention.

SO Sequence 197 AA:

Query Match 12.9%; Score 108; DB 23; Length 197;  
Best Local Similarity 32.4%; Pred. No. 0.0028;

Matches 36; Conservative 16; Mismatches 35; Indels 24; Gaps 5;

QY 8 GSSLIIISVEIVGCAQNFSEYGAFTG-----AVVGVAGOLFSGSRVAMAIIG 59

Db 7 GVVLLASSMALGACANTGT---TGNGTGFSGANVKNKAVIGANAGAL---CGTAISKATGG 60

QY 60 -----AVLGLGSKIGSQMDQDKIKLNLSLEKYKAGQVTRNPDGN 104

Db 61 EKTGRDAIIIGAANVGAAGAAMERQAK----QIEQKQMGTVTHDIDGN 107

RESULT 11

AA020105  
ID AA020105 standard; Protein; 224 AA.

XX  
AC AA020105;

DT 23-APR-2001 (first entry)

DE Moraxella catarrhalis BASB113 protein.

XX  
KW BASB113; infection; otitis media; pneumonia; therapy; diagnosis;

KW antibacterial; antimicrobial.

OS  
XX Moraxella catarrhalis.

PN  
XX WO200100836-A1.

PD  
XX 04-JAN-2001.

PF 23-JUN-2000: 2000MO-EP05851.

XX  
PR 25-JUN-1999: 99GB-0015044.

XX  
PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX  
PI Thonnard J;

XX  
DR WPI; 2001-112458/12.

XX  
DR N-PSDB; AAF30043.

PT New BASB113 polypeptide isolated from Moraxella catarrhalis bacterium,

PT useful for diagnosing and producing vaccines against bacterial

XX infections such as otitis media and pneumonia

PS Claim 1; Page 67; 86pp; English.

XX  
XX The present sequence is that of BASB113 protein from Moraxella

CC catarrhalis strain Mc2931 (ATCC 43617), a causative agent of otitis

CC





OY 13 IISVFLVGCANFSR-----OEVGATGAVVGGVAGQLFGKG--SGRVAMATGCAVIGGI 65  
185 IISILPAKVAVDNSQNKRNAQAFGALIGAVAGCVIGHNVGSGSNSGTTAGAVGGAVGAA 244  
OY 66 IGSKI-----GQSMDOODKIKLNOSLEKVKAGQVT 95  
245 AGSMVNDKTLMEGVSLTYKEGTKVYTSQVGKEFOFT 281  
Db

Search completed: February 12, 2003, 16:43:14  
Job time : 38 secs

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Page 2



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; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP9107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-8

Query Match
Best Local Similarity 20.9%; Score 77.5; DB 4; Length 255;
Pred. No. 0.73;
Matches 37; Conservative 28; Mismatches 81; Indels 31; Gaps 7;

OY 6 LGSSLLIISVFLVGCANFROEVGATGAVY---GGVAGQLFGKSGRVAMATGAV 61
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DB 83 LQMTSLRSEDYAMTYCADDYGAY-WGGGTTVTYSSGGGGSGGGSDIELTQSPAI 141
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 62 LGGLISKIGQSMQODKIK-LN-----QSLEKYKAGQVTRMRNPDTGNSY 106
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 142 MSASPEKEVMTTCASSSVRYMNFQOKSGTSPKRWITDTSKSSGVPAHFGSGGSETSY 201
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 107 SVEPVRYTQRYNKOERROQYCFEFQOKAMT--AGOKQELIYGTACROPDGRWOYISTE 161
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 202 SL-----TISMEADATYTCQOWSNPLTFGAGTKLELKRAAEQ-----KLISSE 249
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 8
US-09-618-869-8
; Sequence 8, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorthée
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP9114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-618-869-8

Query Match
Best Local Similarity 20.9%; Score 77.5; DB 4; Length 255;
Pred. No. 0.73;
Matches 37; Conservative 28; Mismatches 81; Indels 31; Gaps 7;

OY 6 LGSSLLIISVFLVGCANFROEVGATGAVY---GGVAGQLFGKSGRVAMATGAV 61
    ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 83 LQMTSLRSEDYAMTYCADDYGAY-WGGGTTVTYSSGGGGSGGGSDIELTQSPAI 141
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 62 LGGLISKIGQSMQODKIK-LN-----QSLEKYKAGQVTRMRNPDTGNSY 106
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 142 MSASPEKEVMTTCASSSVRYMNFQOKSGTSPKRWITDTSKSSGVPAHFGSGGSETSY 201
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 107 SVEPVRYTQRYNKOERROQYCFEFQOKAMT--AGOKQELIYGTACROPDGRWOYISTE 161
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 202 SL-----TISMEADATYTCQOWSNPLTFGAGTKLELKRAAEQ-----KLISSE 249
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RESULT 9
US-09-067-351-2
; Sequence 2, Application US/09067351
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```

; Patent No. 5994081
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,351
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0511 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 551 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KERANOTO2
; CLONE: 2029060
US-09-067-351-2

Query Match
Best Local Similarity 22.4%; Score 77; DB 2; Length 551;
Pred. No. 2.3;
Matches 28; Conservative 28; Mismatches 53; Indels 16; Gaps 2;

OY 8 GSSLLIISVFLVGCANFROEVGATGAVGVAGQLFGKSGRVAMATGAVIGGLIG 67
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DB 54 GASFSRSLYNLNGAKRVSLNCGSSCSGFGAGRSNFGVNSG---FGYGGVGGGFGSG 110
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 68 SK-----IGQSMQODKIKLNQSLKRYKAGQVTRMRNPDTGNSYSVEPVRTY 114
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 111 PSFPVCPGPGIOEVTVNOSLTLPLHLQIDPTIORVRAEERQIKTLNKKFSLDKVFL 170
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 115 QRYNK 119
    :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 171 EQQNK 175
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RESULT 10
US-09-360-490-2
; Sequence 2, Application US/09360490
; Patent No. 6221843
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Baughn, Mariah
; TITLE OF INVENTION: HUMAN KERATINS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
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:
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/360,490
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: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/067,351
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: CERRONE, MICHAEL C.
: REGISTRATION NUMBER: 39,132
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 845-0555
: TELEFAX: (650) 845-4166
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 551 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: KERNOT02
: CLONE: 2029060
:
: US-09-360-490-2
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: Query Match          9.2%; Score 77; DB 4; Length 551;
: Best Local Similarity 22.4%; Pred. No. 2.3;
: Matches 28; Conservative 28; Mismatches 53; Indels 16; Gaps 2;
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: Oy 8 GSSLIISFVLGCAQNFROEGATGAVGAGVACQLFGKSGRYAMAGAVLGLIG 67
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:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Db 54 GASFGSRSLYINIGAKRYSLNCGSSCRSGFGRASNGFGVSG---FGYGGVGGFSG 110
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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: Oy 68 SK-----IGQMDQDQDKRLKNSLEKRYAGQVTRRNDTGNSTSVYEVRY 114
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: Db 111 PSEFVCPGCGIEVTVNOSLTPHLQIDPTIQRVAEREOIKTLNKFSEIDKVRFL 170
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: Oy 115 QRYNK 119
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Db 171 EQONK 175
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:
: RESULT 11
: US-08-374-077C-2
: Sequence 2, Application US/08374077C
: Patent No. 6027912
: GENERAL INFORMATION:
: APPLICANT: Hall, Linda M.
: APPLICANT: Ren, Dejian
: APPLICANT: Zheng, Wei
: APPLICANT: Dubald, Manuel Marcel Paul
: TITLE OF INVENTION: Genes Encoding an Invertebrate Alpha
: TITLE OF INVENTION: Calcium Channel Subunit
: NUMBER OF SEQUENCES: 57
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314-3187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
:
: US-09-677-374-2.ra1
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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/374,077C
: FILING DATE: 19-JAN-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: McGowan, Malcolm M.
: REGISTRATION NUMBER: 39,300
: REFERENCE/DOCKET NUMBER: 022650-264
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-836-6620
: TELEFAX: 703-836-2021
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2516 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-374-077C-2
:
: Query Match          9.2%; Score 76.5; DB 3; Length 2516;
: Best Local Similarity 24.8%; Pred. No. 20;
: Matches 32; Conservative 18; Mismatches 66; Indels 13; Gaps 4;
:
: Oy 30 VGATGAVGVGVAQGFQKSGRYAMATG--AVLGLIGSKIGOS---MQQDKIKIN 83
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Db 2389 IGSSNGSIFGSGAGLGGAGSGGVC-GLGSSSIRNAGFGSGSPSLSPQHPYSGTIN 2447
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Oy 84 -----QSEKRYKAGQVTRRNDTGNSTSVYEVRYQRYNKQERRQOYCREFOKAMIA 137
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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: Db 2448 SPPIPDNRLRRVATVYTTNNNKSOVSONNSSLVNRAVANSQMNNSPTGPVQOOSPLR 2507
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Oy 138 GQKQEIYGT 146
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
: Db 2508 GQONQYSS 2516
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
:
: RESULT 12
: US-08-895-590-2
: Sequence 2, Application US/08895590
: Patent No. 6207410
: GENERAL INFORMATION:
: APPLICANT: Hall, Linda M.
: APPLICANT: Ren, Dejian
: APPLICANT: Zheng, Wei
: APPLICANT: Dubald, Manuel Marcel Paul
: TITLE OF INVENTION: Genes Encoding an Insect Calcium Channel
: NUMBER OF SEQUENCES: 101
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
: STREET: 699 Prince Street
: CITY: Alexandria
: STATE: VA
: COUNTRY: USA
: ZIP: 22314-3187
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/895,590
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/374,888
: FILING DATE: 19-JAN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: McGowan, Malcolm M.
: REGISTRATION NUMBER: 39,300
: REFERENCE/DOCKET NUMBER: 022650-263
: TELECOMMUNICATION INFORMATION:
:
: US-09-677-374-2.ra1
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OY 121 ERRQ-----QYCREFOQKAMIAQOKOIEYGTAC 148  
 DB 912 NKRNTNRRPDVKEFGGCGIVGCVYLLPRRGPRLGVATRTKTSERSQPRGRPI--PKA 969  
 OY 149 ROPDGR-----MOVISTE 161  
 DB 970 RREGRRTMAQPGYPMPLYGNE 990

RESULT 15

US-08-440-519-12  
 ; Sequence 12, Application US/08440519  
 ; Patent No. 5712087

GENERAL INFORMATION:  
 APPLICANT: Houghton, Michael  
 APPLICANT: Cho, Qui-Lim  
 APPLICANT: Kuo, George  
 TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)  
 TITLE OF INVENTION: Antigens for use in Immunoassays for Anti-HCV Antibodies  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Chiron Corporation  
 STREET: P.O. Box 8097 (Int. Prop. R-440)  
 CITY: Emeryville  
 STATE: CA

COUNTRY: U.S.A.  
 ZIP: 94662-8097

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:

\* APPLICATION NUMBER: US/08/440,519  
 FILING DATE: 12-MAY-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/910,760  
 FILING DATE: 07-JUL-1992

ATTORNEY/AGENT INFORMATION:  
 NAME: Blackburn Esq., Robert P.

REGISTRATION NUMBER: 30,447  
 REFERENCE/DOCKET NUMBER: 0101.002

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (510) 601-2702

TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1021 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-440-519-12

Query Match 9.1%; Score 76; DB 1; Length 1021;  
 Best Local Similarity 20.9%; Pred. No. 6.8;

Matches 42; Conservative 24; Mismatches 63; Indels 72; Gaps 9;

OY 31 GATGAVGVGVGQLFGK-GSGRVMAI-----GCAVLGGLIGSKI--GQSMDOQDKIKLN 83  
 DB 792 GAATAFVAGLAGMAIGSVGLGLVLDILAGYGAGVAGALVAFKINSGEVSTEDLVNLL 851  
 OY 84 QSL-----EKYKGO-VTRMKN-----PDTGNSYSVEPVRTYQRYNKO 120  
 DB 852 PALSLGALVGVCAILIRRHVGPBGAVOMNRLIAFASRGNHVSPGNSSTNPKPKOK 911  
 OY 121 ERRQ-----QYCREFOQKAMIAQOKOIEYGTAC 148  
 DB 912 NKRNTNRRPDVKEFGGCGIVGCVYLLPRRGPRLGVATRTKTSERSQPRGRPI--PKA 969  
 OY 149 ROPDGR-----MOVISTE 161

DB 970 RREGRRTMAQPGYPMPLYGNE 990

Search completed: February 12, 2003, 16:46:34  
 Job time: 32 secs

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[illegible]

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RESULT 3
US-09-981-353-19
: Sequence 19, Application US/09981353
: Patent No. US20020160382A1
: GENERAL INFORMATION:
: APPLICANT: Lasek, Amy W.
: APPLICANT: Jones, David A.
: TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
: FILE REFERENCE: PA-0038 US
: CURRENT APPLICATION NUMBER: US/09/981,353
: CURRENT FILING DATE: 2001-10-11
: NUMBER OF SEQ ID NOS: 194
: SOFTWARE: PERL Program
: SEQ ID NO 19
: LENGTH: 553
: TYPE: PR1
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No. US20020160382A1 3040213CD1
US-09-981-353-19

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Query Match	9.5%	Score 79.5;	DB 9;	Length 553;
Best Local Similarity	25.3%	Fred. No. 2.4;		
Matches	41;	Conservative	20;	Mismatches 54; Indels 47; Gaps 8;
QY	6	LOGSSLIISVFLVCAONFSROEVGA	-----	TGAVVGGVAGOLFGRK 49
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Db	90	VQAEKVEVFSSGLKMGSLNLEPDNGVGVVFGNDKLTREGDIKRTGAIIVPVGE	---	EL 146
QY	50	SGRYAMATIGAVLG-GLIGSK	-----	TGSSMDQDKTKLNSLEKVRQ 93
	:	:	:	:
Db	147	LGRVVDALGNALIDGKGPISGKTRRPFVGLKAPGILPRISVREPMQTGKAVDSLVPITGRQ		206
QY	94	YTRMR-----NPDG-NSYSEVPATQRYN-KQERROQYC		127
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Db	207	-----KELLIGDQGTGKTAIDITTIINOKRFNDSDEKKKLYC		244

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RESULT 4
US-09-925-300-1381      ; Sequence 1381, Application US/09925300
; Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
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NAME/KEY: SITE
LOCATION: (507)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (524)
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LOCATION: (362)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1381

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Query Match	9.4%	Score 79;	DB 10;	Length 618;
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QY	78	DKT-----KLNQSLSEYKA-----	-GQVFWNRPRDGTGNSYSEVPRIQYRNVK	119
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Db	157	EKVTMGNLMDRLASLYLDKVRALAEESNYELEGIKIKENYKHK-GNSHQEP--RDVSKYIK		212
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RESULT 5  
 US-09-815-242-12113  
 : Sequence 12113, Application US/09815242  
 : Patent No. US20020061569A1  
 : GENERAL INFORMATION:  
 : APPLICANT: Haselbeck, Robert  
 : APPLICANT: Ohlsen, Kari L.  
 : APPLICANT: Zyskind, Judith W.  
 : APPLICANT: Wall, Daniel  
 : APPLICANT: Travick, John D.  
 : APPLICANT: Carr, Grant J.  
 : APPLICANT: Yamamoto, Robert T.  
 : APPLICANT: Xu, H. Howard  
 : TITLE OF INVENTION: Identification of Essential Genes in  
 : FILE OF INVENTION: Prokaryotes  
 : FILE REFERENCE: ELITRA.011A  
 : CURRENT APPLICATION NUMBER: US/09/815, 242  
 : CURRENT FILING DATE: 2001-03-21  
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 : PRIOR APPLICATION NUMBER: 60/206, 848  
 : PRIOR FILING DATE: 2000-05-23  
 : PRIOR APPLICATION NUMBER: 60/207, 727  
 : PRIOR FILING DATE: 2000-05-26  
 : PRIOR APPLICATION NUMBER: 60/242, 578  
 : PRIOR FILING DATE: 2000-10-23



APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Thomas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1c11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
PRIOR FILING DATE: 2001-10-15  
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PRIOR FILING DATE: 2001-07-30  
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: PRIOR APPLICATION NUMBER: 60/085697

Query Match      8.9%; Score 74.5; DB 9; Length 285;
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Db 199 GTFVGGLMAFOKYAGETVGERKQKRAKALHEK---LEEMKGRLOVTEHLPRKIESSLR 255
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RESULT 9
US-09-978-697-28
: Sequence 28, Application US/09978697
: Patent No. US20020169284A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi
: APPLICANT: Baker Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleon
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Fong, Sherman
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerber, Hanspeter
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: APPLICANT: Gerltsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
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: APPLICANT: Pan, James
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: APPLICANT: Roy, Margaret Ann
: APPLICANT: Shelton, David L.
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2630PIC27
: CURRENT APPLICATION NUMBER: US/09/978,697
: CURRENT FILING DATE: 2001-10-16
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Query Match  
Best Local Similarity 20.8%; Score 74.5; DB 9; Length 285;  
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D 199 GTVGGILMAFPKAYGETYQERKORRALHELK---LEEKKGLOYTEHLPKRIESSLR 255  
QY 117 YNKE 121  
D 256 EDEPE 260

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; Sequence 28, Application US/09978192A  
; Patent No. US2002017553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC9  
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PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
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PRIOR APPLICATION NUMBER: 60/081070  
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PRIOR FILING DATE: 1998-04-09  
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PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
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PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742

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; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
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; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085339
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
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; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      8.9%: Score 74.5; DB 9; Length 285;
Best Local Similarity 20.8%: Pred. No. 3.4;
Matches 26; Conservative 27; Mismatches 49; Indels 23; Gaps 4;

OY      12  IISVF-LVGCANFSROEVGATGAVGVAGQLFGKSGRYAMATGAVLIGLIGSKI 70
;      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      144  VFTITFTVTSINRYRNKDALSHFVIAGAVTGSLSF-----RINVGRLGVAGIIGALL 198
;      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      71  GQSM-----QQDKIKLQSLSEKYKAGCVTRKRPDPDNGNSVSEPVRYOR 116
;      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      199  GFVGVGLMAFORVAGETVVERKQDKRKALHLEK---LEEMKGRLOVTEHLPKRISSLR 255
;      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY      117  YNKE 121
;      : : : : :
Db      256  EDEPE 260

RESULT 11
US-09-999-832A-28
; Sequence 28, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James J.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/077450
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PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080155
PRIOR FILING DATE: 1998-03-31	PRIOR APPLICATION NUMBER: 60/080194
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PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559
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; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
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Best Local Similarity 20.8%; Pred. No. 3.4;
Matches 26; Conservative 27; Mismatches 49; Indels 23; Gaps 4;
OY    12 IITSVF-LVGCANFNSROEDVGATGAVGVAGOLFGKSGRVAMAGCAVLGLIGLSKI 70
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Db     144 VEVTFNTVNSTSLNYRRKKDALSHFIVAGVGSIF-----RINGLGLVAGCITIGALL 198
OY     71 GOSMD-----QQDKIKLNSLEKVAKGYTRMRNPPTGNSYSVEPRVTYOR 116
       : : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db     199 GPVGGILMAFOKYAGETVOERKQKDRALHELK--LEEMKGRIQVTEHLPDEKIESSLR 255
OY     117 YNKQE 121
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Db     256 EDEPE 260

RESULT 12
US-09-978-189-28
; Sequence 28, Application US/09978189
; Publication No. US20030004102a1
GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen

```

APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC  
CURRENT APPLICATION NUMBER: US/09/978,189  
PRIOR FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
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PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30

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PRIOR FILING DATE: 1998-03-31  
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PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
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PRIOR APPLICATION NUMBER: 60/082704  
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PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
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PRIOR FILING DATE: 1998-04-29  
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PRIOR APPLICATION NUMBER: 60/083554  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083558  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083559  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083500



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Db 199 GTPVGGILMAFOXYAGETVQERKQDRKALHEIK---LEEMKGRLOVTEHLPEKIESSLR 255
QY 117 YNKOE 121
Db 256 EDEPE 260
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## RESULT 15

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US-10-175-737-4
; Sequence 4, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-4
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Query Match 8.9%; Score 74.5; DB 9; Length 285;

Best Local Similarity 20.8%; Pred. No. 3.4; Mismatches 49; Indels 23; Gaps 4;

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Matches 26; Conservative 27; Mismatches 49; Indels 23; Gaps 4;
QY 12 IISVF-LVGCAGNFSRQEVGAATGAVVGAGVAGQLFGKSGRYAMAIGAVLGLIGSKI 70
Db 144 VFVTIETVNTSLNVYRNKDALSHFVIAGAVTSLF-----RINVGRLGLVAGGIIGALL 198
QY 71 GQSMQ-----QQDKIKLNQSLKXKAGQVTRRNPDIGNSYSVEPVFTYQR 116
Db 199 GTPVGGILMAFOXYAGETVQERKQDRKALHEIK---LEEMKGRLOVTEHLPEKIESSLR 255
QY 117 YNKOE 121
Db 256 EDEPE 260
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Search completed: February 12, 2003, 16:50:27  
Job time : 13 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 12, 2003, 16:41:16 : Search time 40 Seconds

(without alignments)  
834.491 Million cell updates/sec

Title: US-09-677-374-2

Perfect score: 836  
Sequence: 1 MNRCLOGSSLIITISVFLVG.....ITGACROPDGRMWISTEK 162

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	836	100.0	162	2	Q9F9K8
2	313.5	37.5	148	2	054381
3	291	34.8	159	2	Q9F9F2
4	266.5	31.9	137	2	052252
5	260.5	31.2	144	2	Q9K2N6
6	259.5	31.0	137	2	031065
7	259.5	31.0	144	2	Q9K4W8
8	252	29.5	151	2	053154
9	247	29.5	151	2	Q9F9Q9
10	237.5	28.4	131	2	Q9F001
11	237.5	28.4	131	2	052637
12	236.5	28.3	131	2	Q9L522
13	223.5	26.7	105	2	031208
14	143	16.7	77	2	Q9AGC7
15	140	16.7	77	2	Q9AGC7
16	131.5	15.7	135	2	08VUE8

17	130.5	15.6	136	16	Q9Z8R9	Q9Z8R9 rhizobium m
18	128.5	15.4	182	16	Q9HX13	Q9HX13 pseudomonas
19	125.5	15.0	131	16	Q8Y6Z7	Q8Y6Z7 brucella me
20	116	13.9	154	16	Q914S1	Q914S1 pseudomonas
21	112	13.4	165	17	Q8YMM1	Q8YMM1 methanocarc
22	112	13.4	257	16	Q9PGX0	Q9PGX0 xylella fas
23	111.5	13.3	142	16	Q8UGR3	Q8UGR3 agrobacteri
24	111	13.3	139	2	Q52854	Q52854 rhizobium l
25	110.5	13.2	232	16	Q9A3X8	Q9A3X8 caulobacter
26	108.5	13.0	135	2	Q9F6B1	Q9F6B1 yersinia pe
27	108.5	13.0	155	16	Q8Z6I6	Q8Z6I6 yersinia pe
28	107.5	12.9	102	16	Q8U5V9	Q8U5V9 agrobacteri
29	107.5	12.9	153	2	Q69776	Q69776 rhizobium e
30	107.5	12.9	155	2	Q9RA95	Q9RA95 serratia sp
31	106.5	12.7	221	16	Q9ZST9	Q9ZST9 rhizobium m
32	106	12.7	135	2	Q9RE08	Q9RE08 peccobacter
33	105.5	12.6	223	2	Q9XC44	Q9XC44 porphyromon
34	102.5	12.3	167	16	Q8Y0Z4	Q8Y0Z4 ralstonia s
35	102	12.2	179	16	Q8XH13	Q8XH13 salmonella
36	102	12.2	232	16	Q8YH11	Q8YH11 brucella me
37	101.5	12.1	304	16	Q91762	Q91762 pseudomonas
38	100	12.0	222	16	Q8XSH0	Q8XSH0 ralstonia s
39	99.5	11.9	83	16	Q92LP2	Q92LP2 rhizobium m
40	99.5	11.9	137	9	Q8SC8K	Q8SC8K pseudomonas
41	99.5	11.9	155	16	Q8XVNB	Q8XVNB pseudomonas
42	99	11.8	154	16	Q9CN83	Q9CN83 pasteurilla s
43	99	11.8	179	16	Q8X8G4	Q8X8G4 escherichia
44	98	11.7	179	16	Q8ZFR7	Q8ZFR7 yersinia pe
45	98	11.7	220	2	Q9XAX8	Q9XAX8 pseudomonas

## ALIGNMENTS

RESULT 1  
Q9F9K8 PRELIMINARY: PRT; 162 AA.  
ID Q9F9K8  
AC Q9F9K8

DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE 17 kDa antigen.

GN OSPA.

OS Piscirickettsia salmonis.

OC Bacteria; Proteobacteria; gamma subdivision; Piscirickettsia group;

OC Piscirickettsia.

OX NCBI\_TaxID=1238;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LF-89;

RA Kuzyn M.A., Burian J., Thornton J.C., Kay W.W.;

RT "Identification of a genus-common Rickettsia surface antigen in the

RT salmonid pathogen Piscirickettsia salmonis.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF184152; AAC17000.1; -  
SQ SEQUENCE 162 AA; 17661 MW; DDEB99E6FD94A527E CRC64;

Query Match 100.0%; Score 836; DB 2; Length 162;

Best Local Similarity 100.0%; Pred. No. 3.7e-68;

Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNRGLOGSSLIITISVFLVCAONFNSROEVGATGAVGVAGOLFPGSGSRVAMATGCA	60
DB	1	MNRGLOGSSLIITISVFLVCAONFNSROEVGATGAVGVAGOLFPGSGSRVAMATGCA	60
QY	61	VLGGLISKTIQSGSDQDDKIKLNOSLEKVRKAGVTRRNRPDTGSSVVEPVRTQRYNKQ	120
DB	61	VLGGLISKTIQSGSDQDDKIKLNOSLEKVRKAGVTRRNRPDTGSSVVEPVRTQRYNKQ	120
QY	121	ERRQGYCREFOQKAMIGOKOEIYGTACROPDGRMWISTEK	162
DB	121	ERRQGYCREFOQKAMIGOKOEIYGTACROPDGRMWISTEK	162

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RESULT 2
ID 054381 PRELIMINARY: PRT: 148 AA.
AC 054381;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE 17 kDa common-antigen (Fragment).
OS Rickettsia sp.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=789;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98087556; PubMed=9425244;
RA Davis M.J., Ying Z., Brunner B.R., Pantloja A., Ferwerda F.H.;
RT "Rickettsial relative associated with papaya bunchy top disease.";
RL Curr. Microbiol. 36:80-84(1998).
DR EMBL: U76907; AAC02809.1; -.
FT NON_TER 1
FT NON_TER 148
SQ SEQUENCE 148 AA; 15050 MW; A7AFEEFE0AEFEAC CRC64;

Query Match
Best Local Similarity 37.5%; Score 313.5; DB 2; Length 148;
Matches 57; Conservative 29; Mismatches 42; Indels 9; Gaps 2;

OY 26 SROEVGAATGAVGVAGVAGOLFEGKSGRYVAMAIGAVLGLGTSKIGSDMDQDK-----IK 81
DB 17 NKQSGGTIGGTLGGSLVSGQSGGGRILAAVAGALLGAILGNIQIGAMDEQDKLAELT 76
OY 82 LKNSLEKAKAGVTRRRNPDTGNSISVEPVRYQRYNKRQOYCREFOQKAMTAGOK 141
DB 77 SORALEAAPSGSSVQWRMPDNGNYGTVPKRAY-----KNTGQYCREYTGTVVVGSKQ 131
OY 142 ELYGTACRQPGRMQVI 158
DB 132 KAYGTACRQPGRMQV 148

RESULT 3
ID 09F9F2 PRELIMINARY: PRT: 159 AA.
AC 09F9F2;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 17 kDa genus-common antigen.
OS Rickettsia felis (Rickettsia azadi).
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=42862;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21217364; PubMed=11321078;
RA Bouyer D.H., Stenos J., Crocquet-Valdes P., Moron C.G., Popov V.L.,
RA Zavala-Velazquez J.E., Foil L.D., Stohard D.R., Azad A.F.,
RA Walker D.H.;
RT "Rickettsia felis: molecular characterization of a new member of the
RT spotted fever group.";
RL Int. J. Syst. Evol. Microbiol. 51:339-347(2001).
DR EMBL: AF195118; AAG28452.1; -.
SQ SEQUENCE 159 AA; 16497 MW; 34C5B020AF470A1F CRC64;

Query Match
Best Local Similarity 34.8%; Score 291; DB 2; Length 159;
Matches 61; Conservative 28; Mismatches 57; Indels 14; Gaps 4;

OY 9 SSLLIISV---FLVGC--AQNFSROEVGAATGAVGVAGVAGOLFEGKSGRYVAMAIGCAVIG 63
DB 5 SKIMTIALASMLQACNGPGCMKNGSTGTLGGAGGALLGSQFGKGGQVGVGVALIG 64
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OY 64 GLISKTIGSDMDQDK-----IKLNSLEKAKAGVTRRRNPDTGNSISVEPVRYQRYNK 119
DB 65 AVLGGQIGAGMDEQDRILAEITSORALEATPSGTSWERNPDNGNHGYVTPNKTY----- 119
OY 120 QERQOYCREFOQKAMTAGOKOELTYGTACRQPGRMQVIS 159
DB 120 RNSTGYCREYTGTVVVGKQKRAYGNACRQPGCLMVOVN 159

RESULT 4
ID 052252 PRELIMINARY: PRT: 137 AA.
AC 052252;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE 17 kDa antigen (Fragment).
OS Rickettsia cooleyi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=69410;
RN [1]
RP SEQUENCE FROM N.A.
RA Billings A.N., Teltow G.J., Walker D.H.;
RT "Molecular characterization of a novel spotted fever group rickettsial
RT species from ixodes scapularis in Texas.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF031534; AAB95267.1; -.
FT NON_TER 1
FT NON_TER 137
SQ SEQUENCE 137 AA; 14215 MW; A27597A9AFD85FC3 CRC64;

Query Match
Best Local Similarity 31.9%; Score 266.5; DB 2; Length 137;
Matches 53; Conservative 23; Mismatches 49; Indels 9; Gaps 2;

OY 23 QNFSROEVGAATGAVGVAGVAGOLFEGKSGRYVAMAIGAVLGLISKTIGSDMDQDK--- 79
DB 7 RGMNKGGTITLGGAGALLGSQFGKQGLVGVAGLILGAILGAGMDEQDRILA 66
OY 80 -IKLNSLEKAKAGVTRRRNPDTGNSISVEPVRYQRYNKRQOYCREFOQKAMTAG 138
DB 67 ELTSORALEAAPSGSSSTEKRRMPDNGNYGTVPNKTY-----RNSTGYCREYTGTVVIG 121
OY 139 QKQELTYGTACRQPD 152
DB 122 KQKRAYGNACRQPD 135

RESULT 5
ID 09K2N6 PRELIMINARY: PRT: 144 AA.
AC 09K2N6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE 17kDa antigen (17 kDa antigen) (Fragment).
OS Male-killing Rickettsia from Adalia bipunctata.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=38026;
RN [1]
RP SEQUENCE FROM N.A.
RA Schlenker H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
RA Bertrand D., Hurst G.D.D., Majerus M.E.N.;
RT "On the evolution of male-killing: Monophyletic origin and horizontal
RT transfer of male-killing Rickettsia (a-Proteobacteria) from two con-
RT generic ladybirds, Adalia bipunctata L. and A. decempunctata L.
RT (Coleoptera: Coccinellidae).";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ269518; CAB96383.1; -.
DR EMBL: AJ269517; CAB96382.1; -.
FT NON_TER 1
FT NON_TER 144
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SO	SEQUENCE	144 AA;	14785 MW;	C8254739CCAS5AE7	CRC64;
QY	26 SROEYGAATGAVGVAGVAGOLFEKSGGRVAMATGAVLGLISKIGQSDQDOK----	IK 81			
Db	17 NKOGTGTLLGGAGGALLSQFGKGGQVLGVGVGALLGAVLGQIAGMDQDRRLAELT	76			
OY	82 LNOSLEKXKAGOVTFMRNPDTCNSYSVEPVRTYQRYNKGQERQOYCREHQOKAMATAGOKO	141			
Db	77 SORALEAPPSGSNVEWRNPDNGNMGVTPPNKTY-----RNSTGYCREYTOTVIVIGKQO	131			
OY	142 EIYGTACROPD 152				
Db	132 KAYGNACROPD 142				
RESULT 6					
O31065	PRELIMINARY;	PRT;	137 AA.		
AC	031065	09M02;			
DT	01-JAN-1998 (TREMBLrel. 05, Created)				
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)				
DT	01-OCT-2001 (TREMBLrel. 18, Last annotation update)				
DE	17 kDa antigen (17 kDa protein) (Fragment).				
OS	Rickettsia honei.				
OC	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;				
CC	Rickettsiaceae; Rickettsiidae; Rickettsia.				
OX	NCBI_TaxID=37816;				
RN	SEQUENCE FROM N.A.				
RP	STRAIN=TT-118;				
RA	Billings A.N., Yu X.-J., Teel P.D., Walker D.H.;				
RL	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.				
RN	(2)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99045882; PubMed=9828442;				
RA	Stenos J., Roux V., Walker D., Rault D.;				
RT	"Rickettsia honei" sp. nov., the aetiological agent of Filanders Island				
RT	spotted fever in Australia."				
RL	Int. J. Syst. Bacteriol. 48:1399-1404(1998).				
DR	EMBL; AF027124; AAB81846.1; -				
DR	EMBL; AF060706; AAD20231.1; -				
DR	EMBL; AF060704; AAD20230.1; -				
FT	NON_TER				
SO	SEQUENCE 137 AA; 14167 MW; 75BC1DD0745B428C CRC64;				
Query Match	31.0%; Score 259.5; DB 2; Length 137;				
Best Local Similarity	39.7%; Pred. No. 5,1e-16;				
Matches	52; Conservative 22; Mismatches 48; Indels 9; Gaps 2;				
OY	26 SROEYGAATGAVGVAGVAGOLFEKSGGRVAMATGAVLGLISKIGQSDQDOK----	IK 81			
Db	10 NKOGTGTLLGGAGGALLSQFGKGGQVLGVGVGALLGAVLGQIAGMDQDRRLAELT	69			
OY	82 LNOSLEKXKAGOVTFMRNPDTCNSYSVEPVRTYQRYNKGQERQOYCREHQOKAMATAGOKO	141			
Db	70 SORALEAPPSGSNVEWRNPDNGNMGVTPPNKTY-----RNSTGYCREYTOTVIVIGKQO	124			
OY	142 EIYGTACROPD 152				
Db	125 KAYGNACROPD 135				
RESULT 7					
O3K4W8	PRELIMINARY;	PRT;	144 AA.		
AC	09K4W8				
DT	01-OCT-2000 (TREMBLrel. 15, Created)				
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				

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DE 17 kDa antigen (Fragment).
OC male-killing Rickettsia from Adalia decempunctata.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=120393;
RN [1]
RP
SEQUENCE FROM N.A.
RX MEDLINE=20575219; PubMed=11133455;
RA Schlenker H.J.G.V.D., Habig M., Sloggett J.J., Webberley M.K.,
RA Bertrand D., Hurst G.D., Majerus M.E.N.;
RT "Incidence of male-killing Rickettsia spp. (alpha-Proteobacteria) in
RT the Ten-Spot Ladybird Beetle Adalia decempunctata L. (Coleoptera:
RT Coccinellidae).";
RL Appl. Environ. Microbiol. 270:270-277(2001).
RL EMBL: AJ269516; CAB6381.1; -.
FT NON_TER 1
FT NON_TER 1
SO SEQUENCE 144 AA; 14801 MW; C825472F16A55AE7 CRC64;

Query Match 31.0%; Score 259.5; DB 2; Length 144;
Best Local Similarity 39.7%; Pred. No. 5.4e-16;
Matches 52; Conservative 22; Mismatches 48; Indels 9; Gaps 2

OY 26 SROEVGATGAVGVAGVAGLFGKSGGRVAMATGAVLGLSIGKIGSQMDQDK---IK 81
DB 17 NKQGTGTLTGAGAGLIGSQFGKGGKQLVGVGVALLGAVGLGQIGAGDDEDRRLAELT 76
OY 82 LMSLEKXKAGQVTRWRNPDGNSYSVEVRYQYRNKERRQYQYCREYQKAMLAGKQ 141
DB 77 SQRALAAPSGSNVEMRNPDNGNHGYVPNKRY-----RNSTGYCREYTVGVIGKQO 131
OY 142 EYGTACRQPD 152
DB 132 KSYGNACRQPD 142

RESULT 8
OY 053154 PRELIMINARY; PRT; 154 AA.
DB 053154
AC 053154.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE (clone PRB F1SF 1), 5' end CDS (Fragment).
OS Rickettsia sp.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=789;
RN [1]
RP
SEQUENCE FROM N.A.
RX MEDLINE=93084757; PubMed=1452660;
RA Baird R.W., Lloyd M., Stenos J., Ross B.C., Stewart R.S., Dwyer B.;
RT "Characterization and comparison of Australian human spotted fever
RT group Rickettsiae.";
RL J. Clin. Microbiol. 30:2896-2902(1992).
RL EMBL: M99391; AAF73386.1; -.
FT NON_TER 154
FT NON_TER 154
SO SEQUENCE 154 AA; 15849 MW; F5C35855EDB8439D2 CRC64;

Query Match 30.1%; Score 252; DB 2; Length 154;
Best Local Similarity 35.5%; Pred. No. 2.8e-15;
Matches 55; Conservative 29; Mismatches 57; Indels 14; Gaps 4

OY 9 SLLIITSV---FLVGC--AQNFSROEVGATGAVGVAGVAGLFGKSGGRVAMATGAVLG 63
DB 5 SKIMITALATSMILQACNGPGGKNNKQGTLLTGAGAGALLGSQFGKGGQLVGVGALLG 64
OY 64 GLIGKIGSQMDQDK---IKLMSLEKXKAGQVTRWRNPDGNSYSVEVRYQYRNK 119
DB 65 AVLQGIQAGMDQDRRLAELTSQRALAAPSGSNVEMRNPDNGSYGVTPNKTYRNSTG 124
OY 120 QERROVYCREFOOKAMLAGOKOIEYGTACRQPDGR 154

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DB 125 QD-----CRVYTOTVIGSKQKQKAYGNACRQPDQ 154

## RESULT 9

Q9F909

ID 09F909 PRELIMINARY: PRT: 151 AA.

AC 09F909: 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE Outer membrane protein (Fragment).  
 OS Rickettsia helvetica.  
 CC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 CC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=35789;

RP SEQUENCE FROM N.A.  
 RA Nilsson K., Pahlson C.;  
 RT "Novel peptide diagnostic reagent and kit for detection of  
 RT rickettsiosis."  
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF181036; AAC09427.1; -.  
 FT NON\_TER 151  
 SQ SEQUENCE 151 AA; 15621 MW; B7407B9C71E4B39 CRC64;

Query Match 29.5%; Score 247; DB 2; Length 151;  
 Best Local Similarity 36.2%; Pred. No. 7.8e-15;  
 Matches 55; Conservative 26; Mismatches 57; Indels 14; Gaps 4;

OY 9 SLLIIISV---FLVGC--AQNFSSROEVGAATGAVVGVAGQDLFGKSGGRVAMAGGAVLG 63  
 DB 5 SKIMIALASMLQACNGPGSMNKGITLLGAGGALLSOGKKGQGLVGVGALLG 64  
 OY 64 GLIGSKIGQSDQDK-----IKLNSLEKVKAGQVTRNPDGNSYSEPVRYGRYRK 119  
 DB 65 AVLGSGQIVAGNDEQDRRLAELTSORALEAPSGSNWERNPDNGHYTPNKTY----- 129  
 OY 120 QERRQGYCRFQOKAMAGOKOETGYACROP 151  
 DB 120 RNSTGQYCREYTOTVIGSKQKQKAYGNACROP 151

## RESULT 10

Q9F001

ID 09F001 PRELIMINARY: PRT: 131 AA.

AC 09F001: 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE 17 kDa protein (Fragment).  
 OS Rickettsia sp. California 2.  
 CC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 CC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=147259;

RP SEQUENCE FROM N.A.  
 RA Raoult D.;  
 RT "A new SFG rickettsia isolated from fleas."  
 RL Submitted (Jan-2001) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CALIFORNIA 2;  
 RA Roux V., Raoult D.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF210693; AAG48554.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 131  
 SQ SEQUENCE 131 AA; 13374 MW; 23C8819B29FF860 CRC64;

Query Match 28.4%; Score 237.5; DB 2; Length 131;  
 Best Local Similarity 37.8%; Pred. No. 4.7e-14;  
 Matches 48; Conservative 22; Mismatches 48; Indels 9; Gaps 2;

OY 26 SROEVGAATGAVVGVAGQDLFGKSGGRVAMAGGAVLGIGLSKIGQSDQDK-----IK 81  
 DB 10 NKQGTGILGGAGGALLGSGFGKKGQGLVGVGALLGAVLGQIGAGNDEQDRRLAELT 69  
 OY 82 LNSLEKVKAGQVTRNPDGNSYSEPVRYGRYRNKQERRQGYCRFQOKAMAGQK 141  
 DB 70 SQRALEATPSGTSEWRNRPNNGHGYTPNKTY-----RNSGQYCREYTOTVIGSKQ 124  
 OY 142 EITGTAC 148  
 DB 125 KAYGNAC 131

## RESULT 11

O52637

ID 052637 PRELIMINARY: PRT: 131 AA.

AC 052637: 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-NOV-1996 (Tremblrel. 08, Last annotation update)  
 DE 17 kDa antigen (Fragment).  
 OS Rickettsia sp.  
 CC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 CC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=789;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94117373; PubMed=8288533;  
 RA Werren J.H., Hurst G.D., Zhang W., Breuwer J.A., Stouthamer R.,  
 RA Majerus M.E.;  
 RT "Rickettsial relative associated with male killing in the ladybird  
 RT beetle (Adalia bipunctata)."  
 RL J. Bacteriol. 176:388-394(1994).  
 DR EMBL: U04162; AAA19235.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 131  
 SQ SEQUENCE 131 AA; 13344 MW; A1DCF71050DF52DF CRC64;

Query Match 28.4%; Score 237.5; DB 2; Length 131;  
 Best Local Similarity 37.8%; Pred. No. 4.7e-14;  
 Matches 48; Conservative 22; Mismatches 48; Indels 9; Gaps 2;

OY 26 SROEVGAATGAVVGVAGQDLFGKSGGRVAMAGGAVLGIGLSKIGQSDQDK-----IK 81  
 DB 10 NKQGTGILGGAGGALLGSGFGKKGQGLVGVGALLGAVLGQIGAGNDEQDRRLAELT 69  
 OY 82 LNSLEKVKAGQVTRNPDGNSYSEPVRYGRYRNKQERRQGYCRFQOKAMAGQK 141  
 DB 70 SQRALEAPSGSNWERNPDNGHGYTPNKTY-----RNSGQYCREYTOTVIGSKQ 124  
 OY 142 EITGTAC 148  
 DB 125 KAYGNAC 131

## RESULT 12

Q9L522

ID 09L522 PRELIMINARY: PRT: 131 AA.

AC 09L522: 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE 17 kDa surface antigen (Fragment).  
 OS Rickettsia peacockii.  
 CC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 CC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=47589;

RP SEQUENCE FROM N.A.  
 RC STRAIN=DAE100R;  
 RX MEDLINE=21091941; PubMed=1157215;  
 RA Simser J.A., Palmer A.T., Munderion U.G., Kurtli T.J.;



"Isolation of a spotted fever group rickettsia, Rickettsia peacockii, in a Rocky Mountain wood tick, Dermacentor andersoni, cell line.";  
RT Appl. Environ. Microbiol. 67:546-552(2001).  
DR EMBL: AF260571; AAF69012.1; -.

FT NON\_TER 131 131  
SQ SEQUENCE 131 AA; 13413 MW; 228C020550CAAD0 CRC64;

Query Match 28.3%; Score 236.5; DB 2; Length 131;  
Best Local Similarity 37.8%; Pred. No. 5.8e-14;  
Matches 48; Conservative 22; Mismatches 48; Indels 9; Gaps 2;

OY 26 SROEVGAATGAVGVAGLGGKSGRVAMAGAVLGLIGSKIGOSMDQDK-----IK 81  
DB 10 NKOGTGLLGAGGALLGSGFGKGGGLGVGVGALLGAVLGGIGAGMDEDRRLAELT 69  
OY 82 LNSGLEVKAGQYTRMRNPOTGNSYSVEPYRTYRKKOERROOYCFEFOOKAMIAQOK 141  
DB 70 SORALETAPSGSNVEMRNPONGNYVTVPNKTY-----RNSGTGYCREYTOTVVGKQO 124

OY 142 EIYGTAC 148  
DB 125 KAYGNAC 131

## RESULT 13

O31208

ID O31208 PRELIMINARY; PRT; 105 AA.

AC O31208;  
DT 01-JUN-1998 (Tremblrel. 05, Created)  
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE 17 kDa antigen (Fragment).  
OS Rickettsia sp. 'La Copita'.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiidae; Rickettsia.  
OX NCBI\_TaxID=69475;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=LA COPITA;  
RX MEDLINE=98367252; PubMed=9701930;  
RA Billings A.N., Yu X.J., Teel P.D., Walker D.H.;  
RT "Detection of a spotted fever group rickettsia in Amblyomma cajennense (Acari: Ixodidae) in south Texas."  
RL J. Med. Entomol. 35:474-478(1998).  
DR EMBL: AF033499; AAB86943.1; -.  
FT NON\_TER 105 105  
SQ SEQUENCE 105 AA; 11236 MW; 7BDD35104701D4FB CRC64;

Query Match 26.7%; Score 223.5; DB 2; Length 105;  
Best Local Similarity 41.2%; Pred. No. 6.6e-13;  
Matches 47; Conservative 17; Mismatches 33; Indels 17; Gaps 3;

OY 43 GOLFSGKSRVAMAGAVLGLIGSKIGOSMDQDK-----IKLNSLEVKAGQYTRMR 98  
DB 3 GQLVGVCV-----CAGLGAVALGGIGAGMDEDRRLAELISQRLAELTAPSGSNVEMR 54  
OY 99 NPDTGNSYSVEPYRTYRKKOERROOYCFEFOOKAMIAQOKETGTACRQDP 152  
DB 55 NPDNGNMGVYTPNKTY-----RNSGTGYCREYTOTVVGKQOKAYGNACRQDP 103

## RESULT 14

Q985G4

ID Q985G4 PRELIMINARY; PRT; 199 AA.

AC Q985G4;  
DT 01-OCT-2001 (Tremblrel. 18, Created)  
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Hypothetical protein mlr7687.  
GN MLR7687.  
Rhlzobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Pyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;

RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=MAFE303099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsuno M., Matsuno A.,  
RA Kouchizuki Y., Nakayama S., Nakazaki N., Shimpso S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."  
RL DNA Res. 7:331-336(2000).

DR EMBL: AP003012; BAB54098.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 199 AA; 20517 MW; 98E6F20A734637AA CRC64;

Query Match 17.1%; Score 143; DB 16; Length 199;  
Best Local Similarity 31.8%; Pred. No. 2.9e-05;  
Matches 35; Conservative 15; Mismatches 50; Indels 10; Gaps 3;

OY 50 SGRVAMAGAVLGLIGSKIGOSMDQDKIKL-----NOSLEVKAGQYTRMRNPOTGNS 105  
DB 92 SGKVTKSIISAMDGGLIGSINGLSDSEKRSALAEAYKALETTTSQKXAMGDOASHY 151  
OY 106 YSVEPYRTYRKKOERROOYCFEFOOKAMIAQOKETGTACRQDPGRW 155  
DB 152 GEVVPAPY-RVGSOD-----CROYTOTVFTGGAGYTRAGTACRNADGSW 195

## RESULT 15

Q9AGC7

ID Q9AGC7 PRELIMINARY; PRT; 77 AA.

AC Q9AGC7;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE 17 kDa antigen (Fragment).  
OS Rickettsia typhi.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiidae; Rickettsia.  
OX NCBI\_TaxID=785;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Paspaliaris V., Liedtke B., Vitella L., Whiting J.L.;  
RT "Rickettsia typhus and Rickettsia felis rickettsioses in Australia."  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF336794; AAK21272.1; -.

FT NON\_TER 77 77  
SQ SEQUENCE 77 AA; 7955 MW; B1E447C037263918 CRC64;

Query Match 16.7%; Score 140; DB 2; Length 77;  
Best Local Similarity 38.7%; Pred. No. 1.6e-05;  
Matches 29; Conservative 13; Mismatches 29; Indels 4; Gaps 1;

OY 43 GOLFSGKSRVAMAGAVLGLIGSKIGOSMDQDK-----IKLNSLEVKAGQYTRMR 98  
DB 3 GSGFGHCKGGLGVGVGALLGAVLGGIGAGMDEDRRLAELISQRLAELTAPSGSNVEMR 62  
OY 99 NPDTGNSYSVEPYRT 113  
DB 63 NPDNGNMGVYTPNKT 77

Search completed: February 12, 2003, 16:45:00  
Job time : 45 secs

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